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OM nucleic - nucleic search, using bw model

Run on: March 4, 2006, 01:46:27 ; Search time 2853.47 Seconds
(without alignments)
295.138 Million cell updates/sec

Title: US-09-701-583A-9
Perfect score: 18
Sequence: 1 cggcatgtctatttgtta 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 106998

Minimum DB seq length: 0
Maximum DB seq length: 4053
Maximum DB seq length: 4053

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	EST:*	EST:*
	1: 9b_est1:*	1: 9b_est1:*
	2: 9b_est2:*	2: 9b_est2:*
	3: 9b_est3:*	3: 9b_est3:*
	4: 9b_htc:*	4: 9b_htc:*
	5: 9b_est4:*	5: 9b_est4:*
	6: 9b_est5:*	6: 9b_est5:*
	7: 9b_est6:*	7: 9b_est6:*
	8: 9b_est7:*	8: 9b_est7:*
	9: 9b_gbs1:*	9: 9b_gbs1:*
	10: 9b_gbs2:*	10: 9b_gbs2:*
	11: 9b_gbs3:*	11: 9b_gbs3:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:*

1: 9b_est1:*

2: 9b_est2:*

3: 9b_est3:*

4: 9b_htc:*

5: 9b_est4:*

6: 9b_est5:*

7: 9b_est6:*

8: 9b_est7:*

9: 9b_gbs1:*

10: 9b_gbs2:*

11: 9b_gbs3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.4	68.9	24	9 AZ846667 2M0146224R	AU258674 AU258674
2	12.4	68.9	34	1 AZ846667 2M0146224R	B2287861 SALK_0212
3	12.4	68.9	37	9 AZ846667 2M0146224R	AZ822722 2M0096008
4	12.4	68.9	40	0 CL313440 mth2-128N	C2463644 c0494-5P
c 5	11.8	65.6	20	10 C2469644	C2477101 d1008-3P
c 6	11.8	65.6	30	10 C2469644	AB081925 Drosophil
c 7	11.8	65.6	37	10 AB081925	C2487985 F0542-3P
c 8	11.6	64.4	29	10 AB081925	AZ402083 1M0162A15
c 9	11.6	64.4	30	10 C2487985	AZ471813 1M0286D06
c 10	11.4	63.3	21	9 AZ471813	AG192945 Pan trogl
c 11	11.4	63.3	28	9 AZ471813	CAB51372 D13A08 A0
c 12	11.4	63.3	31	10 AG192945	AJ587601 Arabidopsis
c 13	11.4	63.3	36	6 CAB51372	BZ768666 SALK_1405
c 14	11.2	62.2	24	10 AJ587601	AI690628 tx9g099.x
c 15	11.2	62.2	27	9 AJ587601	CZ410021 C05477b-5
c 16	11.2	62.2	28	10 CZ410021	AV852639 AV852639
c 17	11.2	62.2	30	10 CZ410021	CZ499987 f07187-5P
c 18	11.2	62.2	34	1 AV852639	/lab_host="E. Coli strain X110-Gold, T1-resistant, F-
c 19	11	61.1	37	10 CZ489987	/clone_lib="Mouse 10kb Plasmid JUGC1M library"
c 20	11	61.1	39	10 AU006827	/note="Vector: PNT42nv; Purified genomic DNA from M.
c 21	10.8	60.0	27	9 AZ478637	AZ478637 1M0298B23
c 22	10.8	60.0	29	9 AZ803680	2M0064009

AU009970 AU009970
AU009989 AU009989
BX532321 Arabidopsis
CA851642 D16A01_B1
AV836794 AV836794
D11885 HUMHMM02G12
N30120 yw63h05_s1
BX661869 Arabidopsis
AZ398982 1M0164D08
AZ767524 1M0566B15
CZ551808 CB2_1687
CZ919151 4021012AO
AL944589 Arabidopsis
AI016852 ou27bd3_x
AI944588 Arabidopsis
CZ559623 PL00353-5
BX336158 Arabidopsis
AZ763574 1M0559P01
AZ768828 1M0563906
CZ467409 C01749-3P
CZ483624 F01137-3P

ALIGNMENTS

RESULT 1
AZ846667

LOCUS 24 bp DNA linear
DEFINITION Mouse 10kb plasmid UGCG2M0146224 R, genomic survey sequence.
ACCESSION AZ846667
VERSION AZ846667.1 GI:13027929
KEYWORDS GSS.
SOURCE ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarctoglires; Glires; Rodentia;
Sciurognath; Murioidea; Muridae; Murinae; Mus.
1 (baes 1 to 24)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beaconn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Neenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederauern,A. and Wright,D. Weiss,R.

AUTHORS TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2006)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@geneitics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: P column: 24
Seq primer: CACAGGGAAACAGGTATGACC
Class: Plasmid ends
High quality sequence stop: 24.
Location/Qualifies
FEATURES Source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGC2M014624"
/sex="Male"
/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb Plasmid JUGC1M library"
/note="Vector: PNT42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://wwwjax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (giga4732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter mouse DNA was annealed to adapter vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGCAGTGTATTTT 15
Db 7 GGCACTTATTGTT 20

RESULT 2
AU258674 LOCUS AU258674 3' -directed mouse cDNA library EST 25-APR-2002
DEFINITION BD00013458 3', mRNA sequence.
ACCESSION AU258674
VERSION AU258674.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathia; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kato, K. and Matoba, R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
891-65 1 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkato@obs.aist-nara.ac.jp/
URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES

Source

Query Match 68.9%; Score 12.4; DB 1; Length 34;
Best Local Similarity 92.9%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

COMMENT

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

891-65 1 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkato@obs.aist-nara.ac.jp/BED/index.html.

Location/Qualifiers

1. .34
/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="BED0013458"

/tissue_type="brain"

/clone_Tib="3"-directed mouse cDNA library"

ORIGIN

Query Match 68.9%; Score 12.4; DB 1; Length 34;

Best Local Similarity 92.9%; Pred. No. 1.8e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ATGGCTPATTTGAA 18

Db 20 ATGGCTPATTTGAA 33

RESULT 3
BZ287861 LOCUS BZ287861 37 bp DNA linear GSS 24-OCT-2002
DEFINITION SALK_021239..53..05..X Arabidopsis thaliana TDNA insertion lines
ORGANISM Arabidopsis thaliana Genomic clone SALK_021239..53..05..X, genomic survey sequence.
ACCESSION BZ287861
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale Cress)
ORGANISM Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eu dicotyledons; core eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 37)
AUTHORS Alonso,J.M., Leise, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
TITLE A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At1g08980.
CLASS: TDNA tagged.
FEATURES Location/Qualifiers
1. .37
/organism="Arabidopsis thaliana"
/mol_type="Genomic DNA"
/ecotype="Col-0"
/clone="SALK_021239..53..05..X"
/clone_xref="taxon:3702"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html"
ORIGIN
Query Match 68.9%; Score 12.4; DB 9; Length 37;
Best Local Similarity 9.9%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GCATGCTATTG 16
Db 22 GCATATCATTG 35
FEATURES Location/Qualifiers
RESULT 4
AZ822722 LOCUS AZ822722 40 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0096008F Mouse 10kb plasmid UGCGJM library Mus musculus genomic clone UGCG2M0096008 F, genomic survey sequence.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Gires; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 40)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

TITLE	Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D. Weiss, R.	AUTHORS	Jakab, J., Deak, G., Kevei, Z., Karchesz, K., Sarai, E., Kiss, P., Kerecz, A., Kalo, P., Endre, G., and Kiss, G.B.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	TITLE	Medicago truncatula BAC end sequencing
COMMENT	[Unpublished (2000)]	JOURNAL	Unpublished (2004)
CONTACT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunin@genetics.utah.edu	COMMENT	Contact: Deak, G. Alfalfa Genomics Group; Medicago Genetics Group Agricultural Biotechnology Center; Biological Research Center P.O. Box 411, Hungary, H-2100 Godollo, Szent Gyorgyi Albert ut 4.; P.O. Box 521, Hungary, H-6701 Szeged, Temesvarj krt. 62 Tel: 36285226142 Fax: 36285226193 Email: gdeak@abc.hu
FEATURES	Insert Length: 10000 Std Error: 0.00 Plate: 0096 row: O column: 08 Seq primer: CGTGTAAACGAGCCGCT Class: Plasmid ends High quality sequence stop: 40 Location/Qualifiers	SOURCE	Plate: 128 row: N column: 01 Seq primer: OP Reverse Class: BAC ends.
FEATURES	1. 40 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="txon:1.0090" /clone="Clone 1.0090" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb Plasmid UGCCM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://wwwjax.org/-resources/documents/dnare/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid pL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	SOURCE	Location/Qualifiers
ORIGIN	Query Match 68.9%; Score 12.4; DB 9; Length 40; Best Local Similarity 92.9%; Pred. No 1.8e+05; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	FEATURES	1. 20 /organism="Medicago truncatula" /mol_type="genomic DNA" /clone_xref="Jemalong" /isolate="A17" /db_xref="Taxon:3880" /sex="Hermaphrodite" /clone_lib="Medicago truncatula BAC end sequences" /note="Organ: Leaf; Vector: pBeloI; Site: HindIII; Site 2: HindIII; Construction of a bacterial artificial chromosome library of Medicago truncatula and identification of clones containing ethylene-response genes. Theor Appl Genet (1999) 98: 638-646 Y.-W. Nam; R.V. Pennetza; G. Endre; P. Uribe; D. Kim; D.R., Cook"
ORIGIN	Query Match 65.6%; Score 11.8; DB 10; Length 20; Best Local Similarity 81.2%; Pred. No 3.6e+05; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	FEATURES	Query Match 65.6%; Score 11.8; DB 10; Length 20; Best Local Similarity 81.2%; Pred. No 3.6e+05; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT	6	DEFINITION	CZ469644-5prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic sequence recovered from 5' end of PiggyBac, genomic survey sequence.
LOCUS	CZ469644	ACCESION	CZ469644
DEFINITION	CZ469644-5prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic sequence recovered from 5' end of PiggyBac, genomic survey sequence.	VERSION	CZ469644.1 GI:62963657
KEYWORDS	GSS	ORGANISM	Drosophila melanogaster (fruit fly)
SOURCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydarioidea; Drosophilidae; Drosophila.	REFERENCE	Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Dembsky,M., Fawcett,R., Francis-Lang,H.L., Ryner,L., Cheung,L.M., Chong,A., Brickson,C., Fisher,W.W., Greer,K., Hartcouni,S.R., Howie,B., Jakkula,L., Joo,D., Kilpatrick,K., Laufer,A., Mazzotta,J.J., Smith,R.D., Stevens,L.M., Stubler,C., Tan,L.R., Ventura,R., Woo,A., Zakrzesk,I., Zhao,L., Chen,F., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
RESULT	5	TITLE	A complementarity transposon tool kit for Drosophila melanogaster using P and piggyBac
LOCUS	CL313440/c	JOURNAL	Nat. Genet. 36 (3) , 283-287 (2004)
DEFINITION	CL313440-OP Medicago truncatula BAC end sequences Medicago truncatula genomic 5', genomic survey sequence.	PUBLISHED	14981521
ACCESSION	CL313440	COMMENT	Contact: Roger A Hoskins Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA Tel: 510 486 4015 Fax: 510 486 6798
VERSION	CL313440.1 GI:44831114	ORGANISM	Medicago truncatula (barrel medic)
SOURCE	Medicago truncatula (barrel medic)	REFERENCE	1 (bases 1 to 20)
ORGANISM	Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Papilionoideae; Trifolieae; Medicago.	REFERENCE	1 (bases 1 to 20)

Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.

Sequence Orientation is forward strand relative to 5' end of piggyBac element.

The piggyBac insertion position is 27 in the 30 bases. This insertion position refers to the first base of the 4 base TRPA target recognition sequence.

Class: transposon insertion site.

Location/Qualifiers

1. .30
organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone lib="Exelixis PiggyBac PB insertions"
/note="Vector: piggyBac PB (GenBank accession number AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp10:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37oC water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dihydronic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN
Query Match 65 6%; Score 11.8; DB 10; Length 30;
Best Local Similarity 86.7%; Pred. No. 3.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCATGTCATTGT 17
Db 12 GCATGTCCTTTT 26

RESULT 8
AB081925_C
LOCUS AB081925 C
DEFINITION Drosophila melanogaster DNA, clone:1(2)SH2 0218, genomic survey sequence.

ACCESSION AB081925
VERSION 1
KEYWORDS GI:21623935
SOURCE GSS
ORGANISM Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.

REFERENCE 1
AUTHORS Oh, S.M., Kingsley,T., Shin,H.H., Zheng,Z., Chen,H.W., Chen,X., Wang,H., Ruan,P., Moody,M. and Hou,S.X.
TITLE A P-element insertion screen identified mutations in 455 novel essential genes in Drosophila Genetics 163 (1), 195-201 (2003)
JOURNAL PUBMED 12586707
PUBLISHED 2 (bases 1 to 29)
REFERENCES 2
AUTHORS Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2002) Suwan Oh, The Laboratory of Immunobiology, National Institutes of Health, National Cancer Institute, Frederick, Maryland 21702-1201, USA
(P-mail):ohsuwandni.ncifcrf.gov, Tel:1-301-846-7314, Fax:1-301-846-6145

FEATURES 1..29
source /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone=1(2)SH2 0218"

COMMENT Contact: Roger A. Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
JOURNAL
PUBLISHED 1.1981521
COMMENT

Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR
Sequence orientation is forward strand relative to 5' end of P element.
The P element insertion position is 1 in the 37 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
CLASS: transposon insertion site.
Location/Qualifiers

FEATURES 1..37
source /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone.lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among insertors hopped onto the Binswanger balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 64.4%; Score 11.6; DB 10; Length 29;
 Best Local Similarity 77.8%; Pred. No. 4.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGATGTCTATTGTA 18
 Db 29 CAGCAGGTCTATTGAA 12

RESULT 9

CZ487985/c CZ487985 30 bp DNA linear GSS 29-APR-2005
LOCUS F05420-3 prime Exelixis piggyBac WH insertions Drosophila
DEFINITION melanogaster genomic sequence recovered from 3' end of piggyBac,
 genomic survey sequence.

ACCESSION C2487985
VERSION C2487985.1
KEYWORDS GI : 62985423
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriodea; Drosophilidae; Drosophila.

REFERENCE I. (bases 1 to 30)
AUTHORS Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
 Singh, C.M., Buchholz, R., Dembsky, M., Fawcett, R., Francis-Lang, H.L.,
 Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
 Greer, K., Hartouni, S.R., Howie, E., Jakkula, I., Joo, D., Killpack, K.,
 Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
 Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
 Swimmer, C.C., Kopczynski, C.C., Duyk, G., Winberg, M.I., and Margolis, J.
 A complementary transposon tool kit for *Drosophila melanogaster*

TITLE Using P and piggyBac

JOURNAL Nat. Genet. 36 (3), 283-287 (2004)

PUBMED 14981521

COMMENT Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798
 Email: RHoskins@lbl.gov

Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of piggyBac element.
 The piggyBac insertion position is 1 in the 30 bases. This insertion position refers to the first base of the 4 base TATA target recognition sequence.
 Class: transposon insertion site.
 Location/Qualifiers 1..30

FEATURES source /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone lib="Exelixis piggyBac WH insertions"
 /note="Vector: piggyBac WH (GenBank accession number AY515148); An isogenic w- *Drosophila melanogaster* strain was mutagenized by remobilization of transposable elements. We remobilized the WH element using the constitutive alpha-1 tubulin/piggyBac transposase source. We remobilized the WH element from a single ammunition element on the Binsinsky balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN Query Match 64.4%; Score 11.6; DB 10; Length 30;

Best Local Similarity 77.8%; Pred. No. 4.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGATGTCTATTGTA 18
 Db 29 CAGCAGGTCTATTGAA 12

RESULT 10

AZ402083 AZ402083 21 bp DNA linear GSS 03-OCT-2000
LOCUS IM0162A15P Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UGGCIM0162A15 F, genomic survey sequence.

DEFINITION AZ402083
ACCESSION AZ402083
VERSION AZ402083.1
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

FEATURES source
 Insert Length: 10000 Std Error: 0.00
 Plate: 0169 row: A column: 15
 Seq primer: CGRTCAAAACGAGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:1090"
 /clone="UGGCIM0162A15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UGGCIM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF122072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 63.3%; Score 11.4; DB 9; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Gaps 0;

Qy 3 GCATGCTATT 15
 ||||| | | | |
 Db 4 GCATTTCTATT 16

RESULT 11

LOCUS AZ471813 28 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0286006R Mouse 10kb plasmid UGCIM library Mus musculus genomic
 clone UGCIM0286D06 R, Genomic Survey sequence.
 ACCESSION AZ471813
 VERSION GI:10629854
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathia; Muridae; Murinae; Mus.
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,,
 Reilly,M., Rose,M., Rose,R., Stoks,R., Tingey,A., von
 Niederhausen,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 RM 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Insert Length: 10000 Std Error: 0.00
 Plate: 0286 row: D column: 06
 Seq primer: CACACAGAACAGCTTATGACC
 Class: Plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1. .28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10900"
 /clone="UGCIM0286D06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lip="Mouse 10kb Plasmid UGCIM library"
 /note="Vector: PWD42nV; Purified Genomic DNA from Mr. Musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnare/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:14732114 [gb AF129072.1]), a copy-number inducible derivative of Plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES source

Qy 4 CATGCTATTGG 16
 ||||| | | | |
 Db 14 CATGCTATTGG 2

RESULT 12

LOCUS AG192945 31 bp DNA linear RP43-069M06-T7, genomic survey sequence.
 DEFINITION AG192945
 ACCESSION AG192945.1
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE 1
 AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Bun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
 TITLE Unpublished (bases 1 to 31)
 JOURNAL Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Bun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
 COMMENT Direct Submission
 Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daegu-si, Korea
 (E-mail: redstone@mail.kribb.re.kr, URL:<http://phs.grc.kribb.re.kr/>
 Tel: 82-42-866-7181, Fax: 82-42-860-1409)
 Clones are derived from the chimpanzee BAC library RP-43. This BAC end was generated during the BAC process and may have higher chance of clone tracking errors.
 PRIMERS Sequencing: T7
 LIBRARY Vector : PBAC3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI
 FEATURES source
 1. .31
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:598"
 /clone="RP43-069M06-T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_id="RP-43 Chimpanzee Male BAC Library"

ORIGIN Query Match 63.3%; Score 11.4; DB 10; Length 31;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TGTCATTGGTA 18
 ||||| | | | |
 Db 17 TGTCATTGGTA 29

RESULT 13

LOCUS CA851372/C
 DEFINITION D13A08 A08 02.ab1 CDNA Peiing library 2, 4 day SCN3 Glycine max
 ACCESSION CA851372
 VERSION CR851372.1 GI:33388165

ORIGIN

KEYWORDS EST
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatozphyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 36)
AUTHORS Alharouf,N., Khan,R. and Matthews,B.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL Genome 47 (2), 380-388 (2004)
PUBMED 160591
COMMENT Contact: Alharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES source
source
1..36
/organism="Glycine max"
/mol_type="mRNA"
/cluTivar="Peking"
/db_xref="taxon:3847"
/clone="D13A08"
/tissue_type="Roots"
/dev_stage="Seedlings"
/note="Vector: PBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN Query Match 63.3%; Score 11.4%; DB 6; Length 36;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 15 CANNCTTATTTTA 1

RESULT 14
LOCUS AJ587601
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
AJ587601_1
ACCESSION AJ587601
VERSION AJ587601_1
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatozphyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Crouaud,C., Derose,R., Pelletier,G.,
Lepaniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 124466565
REFERENCE 2 (bases 1 to 24)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (S) resulting from
the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbscap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French Plant genomics program 'Genoplante' (<http://www.genoplante.com>) and 'Genoplante-info' (<http://genoplante.info>).

FEATURES source
source
1..24
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="298108"
/clone.lib="Arabidopsis thaliana"
/ecotype="Wassilewskija"
/note="T-DNA flanking sequence
left border"

ORIGIN Query Match 62.2%; Score 11.2%; DB 10; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 15
LOCUS BZ768666
DEFINITION SALK_140548_46_70.x Arabidopsis thaliana TDNA insertion lines
survey sequence.
BZ768666
Db 2 GGCGATGTCTATTGTC 17
1 GGC GTGTGTAAATTGTC 16

ORIGIN Query Match 62.2%; Score 11.2%; DB 10; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 15
LOCUS BZ768666
DEFINITION SALK_140548_46_70.x Arabidopsis thaliana TDNA insertion lines
survey sequence.
BZ768666
Db 2 GGCGATGTCTATTGTC 17
1 GGC GTGTGTAAATTGTC 16

ORIGIN Query Match 62.2%; Score 11.2%; DB 10; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 27)
AUTHORS Gadribab,C., Jesie,A., Karres,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J., and Becker,J.R.
TITLE A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
COMMENT Contact: Joseph R. Becker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
CLASS: TDNA tagged.

FEATURES source
source
1..27
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_140548_46_70.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html"

ORIGIN
Query Match Score 11.2; DB 9; Length 27;
Best Local Similarity 81.2%; Pred. No. 7.2e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCATGCTATTTGTA 18
| | | | | | | | | | | | | |
Db 26 GCTTGCTCTTTTTA 11

Search completed: March 4, 2006, 03:39:01
Job time : 2857.47 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
M nucleic - nucleic search, using SW model
run on: March 4, 2006, 01:49:48 ; Search time 375.632 Seconds
(without alignments)
396.263 Million cell updates/sec
Title: US-09-701-583A-9
Perfect score: 18
Sequence: 1 cggcatgtctattttgtta 18
Coring table: IDENTITY_NUC
Gapext 1.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 10900902
Sequence 777184,
Sequence 180128,
Sequence 583979,
Sequence 715766,
Sequence 11172,
Sequence 229607,
Sequence 239950,
Sequence 294363,
Sequence 322759,
Sequence 439359,
Sequence 7, Appli
Sequence 55957, A
Sequence 518120,
Sequence 60048, A
Sequence 589217,
Sequence 592572,
Sequence 808618,
Sequence 51384, A
Sequence 51387, A
Sequence 51389, A
Sequence 51390, A
Sequence 271471,

ALIGNMENTS

ered. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	18	100.0	18	5	US-10-146-058-72	Sequence 72, Appl
2	18	100.0	18	6	US-10-220-033-4	Sequence 4, Appl
3	18	100.0	18	9	US-10-984-919-1209	Sequence 1209, Ap
4	16	88.9	16	9	US-10-984-919-1277	Sequence 1277, Ap
5	16	88.9	20	6	US-10-189-267-40	Sequence 40, Appl
c	6	88.9	20	6	US-10-189-267-185	Sequence 185, Appl
c	6	88.9	20	9	US-10-984-919-529	Sequence 529, App
c	7	88.9	20	6	US-10-189-267-116	Sequence 116, App
c	8	82.2	20	6	US-10-189-267-243	Sequence 243, App
c	9	14.8	82.2	20	6	US-10-189-267-243
c	10	14.8	82.2	25	5	US-10-098-263B-91037
c	11	14.8	82.2	25	10	US-11-036-317-121656
c	12	14.8	82.2	25	10	US-11-060-756-190386
c	13	14.8	82.2	25	10	US-11-060-756-259860
c	14	14.8	80.0	25	8	US-10-719-900-465200
c	15	14.4	80.0	25	10	US-11-036-317-194446
c	16	14.4	80.0	25	10	US-11-036-317-253543
c	17	14.4	80.0	25	10	US-11-036-317-276997
c	18	14.4	80.0	25	10	US-11-036-317-310713
c	19	14.4	80.0	25	10	US-11-036-317-334637
c	20	14.4	80.0	25	10	US-11-036-317-383155
c	21	14	77.8	20	6	US-10-189-267-34
c	22	14	77.8	20	6	US-10-189-467-197
c	23	14	77.8	25	10	US-11-036-317-474175
c	24	14	77.8	25	10	Sequence 474175, Appl
c	25	14	77.8	25	10	Sequence 197, Appl

SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 ANTI-SENSE: YES
 US-10-146-058-72

RESULT 2
 US-10-220-033-4
 / Sequence 4, Application US/102200933
 / Publication No. US2003186906A1
 / GENERAL INFORMATION:
 / APPLICANT: Schlingensiepen, Karl-Hermann
 / TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
 / TITLE OF INVENTION: and a molecule binding to an expression product of that
 / TITLE OF INVENTION: gene
 / FILE REFERENCE: P6819US0
 / CURRENT APPLICATION NUMBER: US/10/220,033
 / CURRENT FILING DATE: 2003-03-17
 / PRIOR APPLICATION NUMBER: PCT/EP01/02694
 / PRIOR FILING DATE: 2001-03-10
 / PRIOR FILING DATE: 2000-03-11
 / NUMBER OF SEQ ID NOS: 42
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 4
 / LENGTH: 18
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: antisense
 / OTHER INFORMATION: Oligonucleotide
 US-10-220-033-4

Query Match 100.0%; Score 18; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 18; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;

Qy 1 CGGCATGTCATTGTGA 18
 Db 1 CGGCATGTCATTGTGA 18

RESULT 3
 US-10-984-919-1209
 / Sequence 1209, Application US/10984919
 / Publication No. US2005013092A1
 / GENERAL INFORMATION:
 / APPLICANT: Schlingensiepen, Karl-Hermann
 / APPLICANT: Brysch, Wolfgang
 / TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 / FILE REFERENCE: 10496/P63763US0
 / CURRENT APPLICATION NUMBER: US/10/984,919
 / CURRENT FILING DATE: 2004-11-10
 / PRIOR APPLICATION NUMBER: US/09/341,700
 / PRIOR FILING DATE: 1999-09-24
 / PRIOR APPLICATION NUMBER: PCT/EP98/00497
 / PRIOR FILING DATE: 1998-01-30
 / PRIOR APPLICATION NUMBER: EP 97 101 531.8
 / PRIOR FILING DATE: 1997-01-31
 / NUMBER OF SEQ ID NOS: 1764
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 1277
 / LENGTH: 16
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence:
 / OTHER INFORMATION: antisense oligonucleotide
 US-10-984-919-1209

Query Match 100.0%; Score 18; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 18; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;

Qy 1 CGGCATGTCATTGTGA 18
 Db 1 CGGCATGTCATTGTGA 18

RESULT 4
 US-10-984-919-1277
 / Sequence 1277, Application US/10984919
 / Publication No. US2005013092A1
 / GENERAL INFORMATION:
 / APPLICANT: Schlingensiepen, Karl-Hermann
 / APPLICANT: Brysch, Wolfgang
 / TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 / FILE REFERENCE: 10496/P63763US0
 / CURRENT APPLICATION NUMBER: US/10/984,919
 / CURRENT FILING DATE: 2004-11-10
 / PRIOR APPLICATION NUMBER: US/09/341,700
 / PRIOR FILING DATE: 1999-09-24
 / PRIOR APPLICATION NUMBER: PCT/EP98/00497
 / PRIOR FILING DATE: 1998-01-30
 / PRIOR APPLICATION NUMBER: EP 97 101 531.8
 / PRIOR FILING DATE: 1997-01-31
 / NUMBER OF SEQ ID NOS: 1764
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 1277
 / LENGTH: 16
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence:
 / OTHER INFORMATION: antisense oligonucleotide
 US-10-984-919-1277

Query Match 100.0%; Score 16; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;

Qy 1 CGGCATGTCATTGTGA 16
 Db 1 CGGCATGTCATTGTGA 16

RESULT 5
 US-10-189-267-40
 / Sequence 40, Application US/10189267
 / Publication No. US20040006030A1
 / GENERAL INFORMATION:
 / APPLICANT: Brett P. Monia
 / APPLICANT: Susan M. Freier
 / APPLICANT: Kenneth W. Dobie
 / TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
 / FILE REFERENCE: PTS-0038
 / CURRENT APPLICATION NUMBER: US/10/189,267
 / CURRENT FILING DATE: 2002-07-02
 / NUMBER OF SEQ ID NOS: 284
 / SEQ ID NO: 40
 / LENGTH: 20
 / TYPE: DNA
 / ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-40

Query Match Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGTCATTCTTG 16
Db 5 CGGCATGTCATTCTTG 20

RESULT 6
US-10-189-267-185/C
Sequence 185, Application US/10189267
Publication No. US20040006030A1

GENERAL INFORMATION:
APPLICANT: Brett P. Monia
ORGANISM: Susan M. Freier
SEQUENCE ID: SEQ ID NO: 185
SEQ ID NO: 185
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-189-267-185

Query Match Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGTCATTCTTG 16
Db 16 CGGCATGTCATTCTTG 1

RESULT 7
US-10-984-919-529
Sequence 529, Application US/10984919
Publication No. US20050130927A1

GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Karl-Hermann
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
FILE REFERENCE: 10496/P63763US0
CURRENT FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US/05/341,700
PRIOR FILING DATE: 1999-09-24
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO: 529
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: antisense oligonucleotide

Query Match Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCATGTCATTCTTGTA 18
Db 1 GCATGTCATTCTTGTA 16

RESULT 8
US-10-189-267-116
Sequence 116, Application US/10189267
Publication No. US20040006030A1

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
FILE REFERENCE: PTS-0038
CURRENT APPLICATION NUMBER: US/10/189,267
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 284
SEQ ID NO: 116
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-116

Query Match Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCATGTCATTCTTGTA 18
Db 1 CGGCATGTCATTCTTGTA 18

RESULT 9
US-10-189-267-243/C
Sequence 243, Application US/10189267
Publication No. US20040006030A1

GENERAL INFORMATION:
APPLICANT: Brett P. Monia
ORGANISM: Susan M. Freier
SEQUENCE ID: SEQ ID NO: 243
SEQ ID NO: 243
TYPE: DNA
ORGANISM: M. musculus
FEATURE:
US-10-189-267-243

Query Match Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCATGTCATTCTTGTA 18
Db 20 CGGCATGTCATTCTTGTA 3

RESULT 10
US-10-038-263B-91037
Sequence 91037, Application US/10098263B
Publication No. US20030104410A1

GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098, 263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIORITY FILING DATE: 2001-03-16
 SEQ ID NO: SSQ ID NOS: 131046
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 91037
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-098-263B-91037

Query Match 82.2%; Score 14.8; DB 5; Length 25;
 Best Local Similarity 88.9%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGATGTCTATTGTAA 18
 Db. 1 CGACATGTCTATTGTAA 18

RESULT 13
 US-11-060-756-259860
 ; Sequence 259860, Application US/11060756
 ; Publication No. US20050221354A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 259860
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 US-11-060-756-259860

Query Match 82.2%; Score 14.8; DB 10; Length 25;
 Best Local Similarity 89.9%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGATGTCTATTGTAA 18
 Db. 8 CGGATGTCTATTGTAA 25

RESULT 14
 US-10-710-900-865662
 ; Sequence 865692, Application US/10719900
 ; Publication No. US2005026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528_1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO: 865692
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-710-900-865662

Query Match 80.0%; Score 14.4; DB 8; Length 25;
 Best Local Similarity 93.8%; Pred. No. 2.5e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATCTCTATTGTAA 18
 Db 10 GCATCTCTATTGTAA 25

RESULT 15
 US-11-036-317-19446/c
 ; Sequence 19446, Application US/11036317
 ; Publication No. US2005021423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 190386
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 US-11-060-756-190386

Query Match 82.2%; Score 14.8; DB 10; Length 25;
 Best Local Similarity 88.9%; Pred. No. 1.5e+03;

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; FILE REFERENCE: 3654_1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 99174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 194446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-194446

Query Match          80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.5e-03;
Matches   15; Conservative
          15; Mismatches  0; Indels  0; Gaps  0;
Qy          3 GCATGCTATTGTGA 18
          ||||| | | | | | |
Db          25 GCATGCTATTGTGA 10
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Search completed: March 4, 2006, 07:04:14
Job time : 375.632 secs

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OM nucleic - nucleic search, using sw mode1

Run on: March 4, 2006, 01:58:42 ; Search time 446.211 Seconds
(without alignments)

88.444 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18

Sequence: 1 cggcatgtctattttgtta 18

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 115814668

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Application NA_New:
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13: /cggn2_6/_ptodata/1/_pubnra/US01 NEW PUB_seq:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	17	94.4	25	12	US-11-121-849-319164	Sequence 31164,
2	17	94.4	25	12	US-11-121-849-319625	Sequence 311625,
3	13.8	76.7	22	8	US-10-310-914A-461071	Sequence 461071,
c 4	13.8	76.7	24	8	US-10-310-914A-378741	Sequence 378741,
c 5	13.4	74.4	22	8	US-11-121-849-151115	Sequence 151115,
6	13.4	74.4	25	12	US-11-121-849-137593	Sequence 137593,
7	13.4	74.4	25	12	US-11-121-849-153313	Sequence 153313,
8	13.4	74.4	25	12	US-11-121-849-153312	Sequence 153312,
9	13.4	74.4	25	12	US-11-121-849-145961	Sequence 145961,
10	13.4	74.4	25	12	US-11-121-849-1437211	Sequence 1437211,
11	13.4	74.4	25	12	US-11-121-849-1437212	Sequence 1437212,
12	13.4	74.4	25	12	US-11-121-849-1437213	Sequence 1437213,
13	13.4	74.4	25	12	US-11-121-849-145961	Sequence 145961,
14	13.2	73.3	25	12	US-11-121-849-1437211	Sequence 1437211,
c 15	13	72.2	19	10	US-11-101-244-1437211	Sequence 1437211,
c 16	13	72.2	19	10	US-11-101-244-1437212	Sequence 1437212,
c 17	13	72.2	19	10	US-11-101-244-1437213	Sequence 1437213,
c 18	13	72.2	19	11	US-11-083-784-1437211	Sequence 1437211,
c 19	13	72.2	19	11	US-11-083-784-1437212	Sequence 1437212,
c 20	13	72.2	19	11	US-11-083-784-1437218	Sequence 1437218,

ALIGNMENTS

RESULT 1
US-11-121-849-319164
; Sequence 31164, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11121-849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 671904
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO: 319164
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-319164

Query Match 94.4%; Score 17; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGATGCTTATTGTGA 18
Db 1 GGCGATGCTTATTGTGA 17

RESULT 2
US-11-121-849-319625
; Sequence 311625, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11121-849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904
i SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
i SEQ ID NO: 319625
i LENGTH: 25
i TYPE: DNA
i ORGANISM: Homo sapien
 US-11-121-849-319625

Query Match 94.4%; Score 17; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCACTCTTATTGTA 18
 Db 1 GGCACTCTTATTGTA 17

RESULT 3
 US-10-310-914A-461071
i Sequence 461071, Application US/10310914A
i Publication No. US2006003322A1

GENERAL INFORMATION:
i APPLICANT: Bentwich, Isaac
i TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and title of invention: uses thereof
i FILE REFERENCE: 06087_0200.CPUS01
i CURRENT APPLICATION NUMBER: US/10/310,914A
i CURRENT FILING DATE: 2002-12-06
i NUMBER OF SEQ ID NOS: 1388402
i SOFTWARE: PatentIn version 3.3
i SEQ ID NO: 461071
i LENGTH: 22
i TYPE: RNA
i ORGANISM: Human
 US-10-310-914A-461071

Query Match 94.4%; Score 17; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCACTCTTATTGTA 18
 Db 1 GGCACTCTTATTGTA 17

RESULT 4
 US-10-310-914A-378741/C
i Sequence 378741, Application US/10310914A
i Publication No. US2006003322A1

GENERAL INFORMATION:
i APPLICANT: Bentwich, Isaac
i TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and title of invention: uses thereof
i FILE REFERENCE: 06087_0200.CPUS01
i CURRENT APPLICATION NUMBER: US/10/310,914A
i CURRENT FILING DATE: 2002-12-06
i NUMBER OF SEQ ID NOS: 1388402
i SOFTWARE: PatentIn version 3.3
i SEQ ID NO: 378741
i LENGTH: 24
i TYPE: RNA
i ORGANISM: Human
 US-10-310-914A-378741

Query Match 94.4%; Score 17; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCACTCTTATTGTA 18
 Db 17 GGCACTCTTATTGTA 1

RESULT 5
 US-10-310-914A-1375953/C
i Sequence 1375953, Application US/10310914A
i Publication No. US2006003322A1

GENERAL INFORMATION:
i APPLICANT: Shiller, Kvuzt
i TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and title of invention: uses thereof
i FILE REFERENCE: 06087_0200.CPUS01
i CURRENT APPLICATION NUMBER: US/10/310,914A
i CURRENT FILING DATE: 2002-12-06
i NUMBER OF SEQ ID NOS: 1388402
i SOFTWARE: PatentIn version 3.3
i SEQ ID NO: 1375953
i LENGTH: 22
i TYPE: RNA
i ORGANISM: Human
 US-10-310-914A-1375953

Query Match 74.4%; Score 13.4; DB 8; Length 22;
 Best Local Similarity 93.3%; Pred. No. 1.e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCACTCTTATTGTA 16
 Db 22 GCCATGTCTATTG 8

RESULT 6
 US-11-121-849-151115
i Sequence 151115, Application US/11121849
i Publication No. US2005027208A1

GENERAL INFORMATION:
i APPLICANT: John Palma
i TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

Query Match 74.4%; Score 13.4; DB 8; Length 22;
 Best Local Similarity 93.3%; Pred. No. 1.e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCACTCTTATTGTA 16
 Db 22 GCCATGTCTATTG 8

RESULT 7
 US-11-136-527-153306
i Sequence 153306, Application US/11136527
i Publication No. US2005287570A1

GENERAL INFORMATION:
i APPLICANT: Wyech
i TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

Query Match 74.4%; Score 13.4; DB 12; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CATTGCTATTGTA 18
 Db 1 CATGCTAGTTGTA 15

RESULT 8
 US-11-136-527-153306
i Sequence 153306, Application US/11136527
i Publication No. US2005287570A1

GENERAL INFORMATION:
i APPLICANT: Mounts, William M
i TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

Query Match 76.7%; Score 13.8; DB 8; Length 24;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCACTCTTATTGTA 18
 Db 17 GGCACTCTTATTGTA 1

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; PRIORITY FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 153306
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-153306

Query Match      74.4%; Score 13.4%; DB 12%; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   3 GCATGCTATTGTG 17
Db   1 GCATGCTATTGTG 15

RESULT 8
US-11-136-527-153312
Sequence 153312, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
; APPLICANT: Wyeth
; ATTORNEY: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 153312

Query Match      74.4%; Score 13.4%; DB 12%; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   3 GCATGCTATTGTG 17
Db   2 GCATGCTATTGTG 16

RESULT 11
US-11-136-527-153325
Sequence 153325, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
; APPLICANT: Wyeth
; ATTORNEY: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 153325

Query Match      74.4%; Score 13.4%; DB 12%; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   3 GCATGCTATTGTG 17
Db   3 GCATGCTATTGTG 17

RESULT 9
US-11-136-527-153313
Sequence 153313, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
; APPLICANT: Wyeth
; ATTORNEY: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 153313

Query Match      74.4%; Score 13.4%; DB 12%; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   3 GCATGCTATTGTG 17
Db   10 GCATGCTATTGTG 24

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RESULT 12
 US-11-136-527-153326
 / Sequence 153326, Application US/11136527
 / Publication No. US20050287570A1
 / GENERAL INFORMATION:
 / APPLICANT: Mounts, William M
 / FEATURE: Wyeth
 / TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 / FILE REFERENCE: 031896-041000 (AM101086)
 / CURRENT APPLICATION NUMBER: US/11/136,527
 / CURRENT FILING DATE: 2005-05-25
 / LENGTH: 25
 / PRIORITY APPLICATION NUMBER: US 60/574,294
 / PRIOR FILING DATE: 2005-05-26
 / NUMBER OF SEQ ID NOS: 362830
 / SOFTWARE: Patentin version 3.2
 / SEQ ID NO: 153326
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Artificial
 / OTHER INFORMATION: Probe
 US-11-136-527-153326

Query Match 74.4%; Score 13.4; DB 12; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.4e-03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Software: Microarray Probe Sequence Listing Generator v 1.1
 SEQ ID NO: 245961
 LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Homo sapien
 US-11-121-849-245961

RESULT 13
 US-11-136-527-153341
 / Sequence 153341, Application US/11136527
 / Publication No. US20050287570A1
 / GENERAL INFORMATION:
 / APPLICANT: Mounts, William M
 / FEATURE: Wyeth
 / TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 / FILE REFERENCE: 031896-041000 (AM101086)
 / CURRENT APPLICATION NUMBER: US/11/136,527
 / CURRENT FILING DATE: 2005-05-25
 / PRIORITY APPLICATION NUMBER: US 60/574,294
 / PRIOR FILING DATE: 2005-05-26
 / NUMBER OF SEQ ID NOS: 362830
 / SOFTWARE: Patentin version 3.2
 / SEQ ID NO: 153341
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Artificial
 / OTHER INFORMATION: Probe
 US-11-136-527-153341

Query Match 74.4%; Score 13.4; DB 12; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.4e-03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Software: Microarray Probe Sequence Listing Generator v 1.1
 SEQ ID NO: 245961
 LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Homo sapien
 US-11-121-849-245961

RESULT 14
 US-11-121-849-245961
 / Sequence 245961, Application US/11121849
 / Publication No. US20050272080A1
 / GENERAL INFORMATION:
 / APPLICANT: John Palma
 / TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: March 4, 2006, 01:38:40 ; Search time 350.053 Seconds
(without alignments)
342.704 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18

Sequence: 1 cggatgtctatttgta 18

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4598950

Minimum DB seq length: 0

Maximum DB seq length: 405

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 1: genesegn1980s:
 2: genesegn1980s:
 3: genesegn2000s:
 4: genesegn2001as:
 5: genesegn2001bs:
 6: genesegn2002as:
 7: genesegn2002bs:
 8: genesegn2003as:
 9: genesegn2003bs:
 10: genesegn2003cs:
 11: genesegn2003ds:
 12: genesegn2004as:
 13: genesegn2004bs:
 14: genesegn2005s:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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3	18	100.0	4	AAD18718	Human oil	
4	18	100.0	18	14	AB01186	TGF-beta
5	18	100.0	22	AAZ65511	Immunosup	
6	18	100.0	27	5	AAF82681	Human TGF
7	16	88.9	16	3	AAZ65472	Immunosup
8	16	88.9	20	2	AAY48940	TGF-beta2
9	16	88.9	20	3	AAZ65448	Immunosup
10	16	88.9	20	3	AaZ65509	Immunosup
C 11	16	88.9	20	12	AD180184	Human tra
C 12	16	88.9	20	12	AD180039	Human tra
C 13	16	88.9	20	14	AB01185	TGF-beta
C 14	14.8	82.2	20	12	AD180242	Mouse tra
C 15	14.8	82.2	20	12	AD180115	Mouse tra
C 16	14.8	82.2	25	9	ACI91046	Human mic
C 17	14.4	80.0	17	2	AAK23221	Integrin
C 18	14	77.8	17	2	AAK23222	Integrin
C 19	14	77.8	20	12	AD180053	Human tra

ALIGNMENTS

RESULT 1	AAQ78423	standard; DNA; 18 BP.	
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AC	AAQ78423;		XX
DT	25-MAR-2003	(revised)	DT
DT	27-JUN-1995	(first entry)	XX
DE	TGF-beta gene phosphorothioate antisense oligonucleotide.		XX
XX	Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;		XX
KW	angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;		KW
KW	carcinogenesis; carcinoma; oesophagus; oesophageal; oesophageal; gut;		KW
KW	immunosuppression; oligonucleotide; ss.		KW
OS	Synthetic.		XX
PN	WO9425588-A2.		XX
XX	WO9425588-A2.		XX
PD	10-NOV-1994.		XX
PF	29-APR-1994;	94WO-EP001362.	PF
XX			XX
PR	30-APR-1993;	93EP-00107089.	PR
PR	13-MAY-1993;	93EP-00107849.	PR
XX			XX
PA	(BIOG-) BILOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.		PA
XX			XX
PI	Schlingensiepen G, Brysch W, Schlingensiepen K,		PI
PI	Bogdahn U;		PI
XX			XX
DR	WPI; 1994-358266/44.		DR
XX			XX
PT	New transforming growth factor beta anti:sense oligo:nucleotide(s) - for		PT
PT	treating immunosuppression, tumours, etc.		PT
PS	Claim 6; Page 44; 74pp; English.		PS
XX			XX
CC	The antisense oligonucleotides are useful in the treatment of tumours in		CC
CC	which expression of TGF-beta is of relevance for pathogenicity and/or		CC
CC	inhibition of pathological angiogenesis. They are used especially for the		CC

colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas. The Oligonucleotides most of which are directed against TGFbeta or VEGF, are inhibitors of monocyte chemotactic protein-1 (MCP-1) and are useful as anti-inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, Glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque

CC oligonucleotide useful in drug target validation
 XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCATGTTATTGTGA 18
 Db 1 CGGCATGTTATTGTGA 18

RESULT 5

AZ65511

ID AZ65511 standard; DNA; 22 BP.

XX AZ65511;

XX 30-MAR-2000 (first entry)

AC DT XX

AC DE XX

DE KW XX

KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; Cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; SS; atherosclerosis.

KW XX Unidentified.

OS OS XX

PN PN WO9963975-A2.

PN XX

PD PD 16-DEC-1999.

PD XX

PF PF 10-JUN-1999;

PF XX 10-JUN-1998;

PR PR 25-JUL-1998;

PR XX 98EP-00110709;

PR XX 98EP-00113974.

(BIOG-) BIOMOLEKULARE DIAGNOSTIK.

PA PA XX

PI PI Schlingensiepen K, Schlingensiepen R, Brysch W;

PI XX DR WPI; 2000-097470/08.

XX DR PT Composition containing immune stimulant and inhibitor of agent that

PT adversely affects the immune response, for treating cancers and

PT infections.

XX XX Claim 10; Fig 1; 30pp; English.

PS PS XX

Pharmaceutical composition useful for treating neoplasm, comprises
 PT stimulators stimulating function of immune system and/or immune cells and
 PT substances inhibiting cell proliferation and/or inducing cell death.
 XX XX

Claim 4; SEQ ID NO 30; 46pp; English.

The invention relates to a pharmaceutical composition (PC) comprising one or more stimulators that stimulate the function of immune system and/or immune cells and one or more substances inhibiting cell proliferation and/or inducing cell death. A pharmaceutical composition is useful for treating neoplasms chosen from solid tumors; blood born tumors such as leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma, carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal carcinoma, epithelial carcinoma, esophageal carcinoma, cervical carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma, gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell carcinoma, bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma, papillary carcinoma, papillary adenocarcinoma, prostrate carcinoma, small intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence represents a TGF-beta 2 inhibition oligonucleotide.

XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

SQ Sequence 18 BP; 4 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 3; Length 22;

SQ Best Local Similarity 100.0%; Pred. No. 26;

Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCATGCTTATTGTGA 18

Db 1 CGGCATGCTTATTGTGA 18

RESULT 5

AZ65511

ID AZ65511 standard; DNA; 22 BP.

XX AZ65511;

XX 30-MAR-2000 (first entry)

AC DT XX

AC DE XX

DE KW XX

KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; Cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; SS; atherosclerosis.

KW XX Unidentified.

OS OS XX

PN PN WO9963975-A2.

PN XX

PD PD 16-DEC-1999.

PD XX

PF PF 10-JUN-1999;

PF XX 10-JUN-1998;

PR PR 25-JUL-1998;

PR XX 98EP-00110709;

PR XX 98EP-00113974.

(BIOG-) BIOMOLEKULARE DIAGNOSTIK.

PA PA XX

PI PI Schlingensiepen K, Schlingensiepen R, Brysch W;

PI XX DR WPI; 2000-097470/08.

XX DR PT Composition containing immune stimulant and inhibitor of agent that

PT adversely affects the immune response, for treating cancers and

PT infections.

XX XX Claim 10; Fig 1; 30pp; English.

PS PS XX

Pharmaceutical composition useful for treating neoplasm, comprises
 PT stimulators stimulating function of immune system and/or immune cells and
 PT substances inhibiting cell proliferation and/or inducing cell death.

XX XX

Claim 4; SEQ ID NO 30; 46pp; English.

PS PS XX

The invention relates to a pharmaceutical composition (PC) comprising one or more stimulators that stimulate the function of immune system and/or immune cells and one or more substances inhibiting cell proliferation and/or inducing cell death. A pharmaceutical composition is useful for treating neoplasms chosen from solid tumors; blood born tumors such as leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma, carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal carcinoma, epithelial carcinoma, esophageal carcinoma, cervical carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma, gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell carcinoma, bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma, papillary carcinoma, papillary adenocarcinoma, prostrate carcinoma, small intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence represents a TGF-beta 2 inhibition oligonucleotide.

XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

SQ Sequence 18 BP; 4 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 3; Length 22;

SQ Best Local Similarity 100.0%; Pred. No. 26;

Sequence 27 BP; 5 A; 7 C; 6 G; 9 T; 0 U; 0 Other;
Q Query Match 100.0%; Score 18; DB 5; Length 27;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 CGGCATGTCATTGTG 16
 1 CGGCATGTCATTGTG 16
 3 CGGCATGTCATTGTG 20

Sequence 16 BP; 2 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
Q Query Match 88.9%; Score 16; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 CGGCATGTCATTGTG 16
 1 CGGCATGTCATTGTG 16

XX AAV48940; DT 30-MAR-2000 (first entry)

AC XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-8.

XX DT XX KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;

DE KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;

XX KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;

KW monocytic chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;

XX KW glomerulonephritis; acute respiratory distress syndrome; ss;

KW atherosclerosis.

OS XX Unidentified.

OS OS Unidentified.

PN XX WO9963975-A2.

XX PN WO9963975-A2.

PD XX PD 16-DEC-1999.

XX PP 99WO-EP004013.

PP 10-JUN-1999;

XX PR 98EP-00110709.

PR 10-JUN-1998;

XX PR 98EP-00113974.

PR 25-JUL-1998;

PA XX (BIOG-) BIOPHYSIK GES BIOMOLEKULARE DIAGNOSTIK.

PA PA

XX PI Schlingensiepen K, Schlingensiepen R, Brysch W;

XX DR WPI; 2000-097470/08.

XX PT Composition containing immune stimulant and inhibitor of agent that

PT adversely affects the immune response, for treating cancers and

PT infections.

XX PS Claim 5; Fig 1; 30pp; English.

XX CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor beta, vascular endothelial growth factor VEGF, interleukin-10 IL-10, Prostaglandin E2 PGs2, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the treatment of neoplasms and infections, particularly hyperproliferation, leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas. The oligonucleotide, most of which are directed against TGFbeta or VEGF, are inhibitors of monocytic chemoattractant protein-1 (MCP-1) and are useful as anti-inflammatory agents for the treatment e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque

XX SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

XX Qy Query Match 88.9%; Score 16; DB 2; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB Qy 3 GCATGTCATTGTGA 18

DB 1 GCATGTCATTGTGA 16

DB RESULT 10

DB AAZ65509

ID AAZ65509 standard; DNA; 20 BP.

ID AAZ65509

XX AC AAZ65509;

XX DT 30-MAR-2000 (first entry)

XX XX

KW	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW	cystosolic; nontropic; neuroprotective; immunosuppressive;
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW	immune; ss; human.
XX	OS
XX	Homo sapiens.
XX	US2004006030-A1.
PN	US2004006030-A1.
PD	08-JAN-2004.
XX	PF 02-JUL-2002; 2002US-00189267.
XX	PR 02-JUL-2002; 2002US-00189267.
PA	(ISIS-) ISIS PHARM INC.
XX	Monia BP, Freier SM, Dobbie KW;
PI	XXX
DR	WPI; 2004-081742/08.
XX	New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.
XX	Example 16; SEQ ID NO 185; 135pp; English.
PS	CC The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and CC inhibits the expression of TGF-beta 2. The invention further relates to: CC a compound 8-80 nucleobases in length that specifically hybridizes with CC at least one 8-nucleobase portion of an active site on a nucleic acid CC molecule encoding TGF-beta 2; a composition comprising the compound and a CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or CC tissues by contacting the cells or tissues with the compound so that CC expression of TGF-beta 2 is inhibited; treating an animal having a CC disease or condition associated with TGF-beta 2 by administering to the CC animal a therapeutic or prophylactic amount of the compound so that CC expression of TGF-beta 2 is inhibited; and screening an antisense CC compound. The antisense compound has cytotoxic, nontropic, CC neuroprotective, and immunosuppressive activities. The compound, CC composition and methods are useful for treating a disease or condition CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g. CC cancer, a neurodegenerative disorder, or a disease or condition involving CC hyperactivation of an immune response. This polynucleotide sequence CC represents a preferred target DNA region of TGF-beta 2 of the invention.
SQ	XX Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
	Query Match Score 16; DB 12; Length 20;
	Best Local Similarity 100.0%; Pred. No. 2.7e-02;
	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 CGGCATGCTATTGTG 16
Db	16 CGCCATGCTATTGTG 1
RESULT 12	
ADI80039	
XX	ID ADI80039 standard; DNA; 20 BP.
XX	AC ADI80039;
DT	22-APR-2004 (first entry)
XX	Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 40.
XX	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX	cystosolic; nontropic; neuroprotective; immunosuppressive;
XX	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX	immune; ss; human.

KW immune; **ss**; human.
 XX PN WO2005059133-A2.
 OS XX
 Homo sapiens.
 XX PD 30-JUN-2005.
 PN 20-DEC-2004; 2004WO-EP053604.
 XX PF
 PD 08-JAN-2004.
 XX PR 19-DEC-2003; 2003EP-00029367.
 XX PR 05-FEB-2004; 2004US-0541771P.
 XX PA (ANTI-) ANTISENSE PHARMA GMBH.
 XX PA
 PR 02-JUL-2002; 2002US-00189267.
 XX PI Schlingensiepen K, Schlingensiepen R;
 PA XX
 (ISIS-) ISIS PHARM INC.
 XX PI SEQ ID NO 29; 46pp; English.
 XX DR 2005-479334/48.
 XX PT Pharmaceutical composition useful for treating neoplasm, comprises
 PT stimulators stimulating function of immune system and/or immune cells and
 PT substances inhibiting cell proliferation and/or inducing cell death.
 XX PS Claim 4; SEQ ID NO 29; 46pp; English.
 XX
 The invention relates to a pharmaceutical composition (PC) comprising one
 CC or more stimulators that stimulate the function of immune system and/or
 CC immune cells and one or more substances inhibiting cell proliferation
 CC and/or inducing cell death. A pharmaceutical composition is useful for
 CC treating neoplasms chosen from solid tumors; blood born tumors such as
 CC leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor
 CC metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder
 CC carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma, cervical
 CC carcinoma of kidney, choriocarcinoma, cyr adenocarcinoma, embryonal
 CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical
 CC carcinoma colon carcinoma, colorectal carcinoma, endometrial carcinoma,
 CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver
 CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell
 CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma,
 CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, small
 CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin
 CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell
 CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine
 CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence
 CC represents a TGF-beta 2 inhibition oligonucleotide.
 XX SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
 XX SQ Sequence Match 88.9%; Score 16; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Query Match 3 GCATGCTTATTGTA 18
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 RESULT 14
 ADI80242/C
 ID ADI80242 standard; DNA; 20 BP.
 XX AC ADI80242;
 AC DT 22-APR-2004 (first entry)
 XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 243.
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cyclostatic; nontropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; **ss**; mouse; murine.
 XX OS Mus musculus.
 XX PN US2004006030-A1.
 XX XX
 DE PD 08-JAN-2004.

XX 08-SBP-2005 (first entry)
 XX TGF-beta 2 inhibition oligonucleotide SEQ ID NO 29.
 XX DE
 KW pharmaceutical; cell death; neoplasm; **ss**; Cytostatic; Apoptotic;
 KW Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
 KW TGF-beta antagonist; Vaccine.
 XX OS Synthetic.

XX 02-JUL-2002; 2002US-00189267.
 PP PR 02-JUL-2002; 2002US-00189267.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Freier SM, Dobie KW;
 XX DR WPI, 2004-081742/08.
 XX PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.
 XX PS Example 16; SEQ ID NO 116; 135pp; English.
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent, inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, nootropic, neuroprotective, and immunosuppressive activities. The compound composition and methods are useful for treating disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.
 XX SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
 XX Query Match Score 14.8%; DB 12; Length 20;
 XX Best Local Similarity 82.2%; Pred. No. 1.1e+03;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX QY 1 CGGCATGTCATTGTTGTA 18
 XX Db 20 CGGCATGTCATTGTTGTA 3
 XX Search completed: March 4, 2006, 02:31:45
 XX Job time : 353.053 secs

RESULT 15
 ADI80115
 ID ADI80115 standard; DNA; 20 BP.
 XX AC ADI80115;
 XX DT 22-APR-2004 (first entry)
 XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 116.
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytosatic; nootropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 OS Mus musculus.
 PN US200406030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:42:16 ; Search time 957.368 Seconds
(without alignments)

1187.494 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gctttcacaaatggaaagc 20

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1934910

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBmbl:
 1: gb_ba:
 2: gb_in:
 3: gb_env:
 4: gb_om:
 5: gb_ov:
 6: gb_pat:
 7: gb_ph:
 8: gb_pr:
 9: gb_ro:
 10: gb_sts:
 11: gb_sy:
 12: gb_un:
 13: gb_vl:
 14: gb_hgt:
 15: gb_pl:
 %

Result No. Score Match Length DB ID Description

1	20	100.0	20	6	A88384 Sequence 53
2	20	100.0	20	6	A90351 Sequence 53
3	20	100.0	20	6	BD065897 An antisense
4	20	100.0	20	6	BD234910 A method
5	20	100.0	20	6	CS123684 Sequence
6	20	100.0	20	6	AX008981 Sequence
7	20	100.0	20	6	AX252495 Sequence
8	18	90.0	18	6	A89125 Sequence 12
9	18	90.0	18	6	BD066638 An antisense
10	18	90.0	18	6	BD234924 A method
11	18	90.0	18	6	AX008995 Sequence
12	16	80.0	16	6	A89127 Sequence 12
13	16	80.0	16	6	BD066640 An antisense
14	16	80.0	16	6	BD234926 A method
15	16	80.0	16	6	AX008997 Sequence
16	16	80.0	18	6	A40542 Sequence 79
17	16	80.0	18	6	A89067 Sequence 12
18	16	80.0	18	6	BD066680 An antisense

ALIGNMENTS

RESULT 1

LOCUS A88384 Sequence 532 from Patent WO9833904.

DEFINITION 20 bp DNA

ACCESSION A88384

VERSION 1 GI:6736954

KEYWORDS unclassified sequences.
1 (bases 1 to 20)

ORGANISM Brysch, W. and Schlingensiepen, K.

REFERENCE 1 (bases 1 to 20)

AUTHORS AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

TITLE Patent: WO 9833904-A 532 - 6 AUG 1998;

JOURNAL BIOGNOSTIK GBS (DE); BRYNSCH WOLFGANG (DE)

FEATURES Location,Qualifiers 1..20

source /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match Best Local Similarity 100.0%; Pred: No. 41; Mismatches 0; MisMatches 0; Indels 0; Gaps 0;

Matchers 20; Conservative 0; Version 1

RESULT 2

LOCUS A90351 Sequence 532 from Patent EP0856579.

DEFINITION 20 bp DNA

ACCESSION A90351

VERSION 1 GI:6738865

KEYWORDS unclassified sequences.
unidentified
ORGANISM unclassified sequences.

SUMMARIES

RESULT 3

Score Match Length DB ID Description

1	20	100.0	20	6	A88384 Sequence 53
2	20	100.0	20	6	A90351 Sequence 53
3	20	100.0	20	6	BD065897 An antisense
4	20	100.0	20	6	BD234910 A method
5	20	100.0	20	6	CS123684 Sequence
6	20	100.0	20	6	AX008981 Sequence
7	20	100.0	20	6	AX252495 Sequence
8	18	90.0	18	6	A89125 Sequence 12
9	18	90.0	18	6	BD066638 An antisense
10	18	90.0	18	6	BD234924 A method
11	18	90.0	18	6	AX008995 Sequence
12	16	80.0	16	6	A89127 Sequence 12
13	16	80.0	16	6	BD066640 An antisense
14	16	80.0	16	6	BD234926 A method
15	16	80.0	16	6	AX008997 Sequence
16	16	80.0	18	6	A40542 Sequence 79
17	16	80.0	18	6	A89067 Sequence 12
18	16	80.0	18	6	BD066680 An antisense

REFERENCE	1	(bases 1 to 20)		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
AUTHORS	Brysch, W.D.	and Schlingensiepen, K.H.		Hominidae; Homo;
TITLE	An antisense Oligonucleotide Preparation method		1 (bases 1 to 20)	
JOURNAL	Patent: EP 08565797-A 532 05-AUG-1998;		Schlingensiepen, K.H., Schlingensiepen, R. and Brysch, W.	
FEATURES	BIOGNOSTIK GES (DE)		A method for stimulating the immune system	
LOCATION/Qualifiers			Patent: JP 2002517434-A 14 18-JUN-2002;	
COMMENT	1.. .20		BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH	
SOURCE	/organism="unidentified"		OS	Homo sapiens (human)
/atom type="unassigned DNA"			PN	JP 2002517434-A/14
/db_xref="taxon:32644"			PD	18-JUN-2002
ORIGIN			PF	10-JUN-1998 JP 2000553044
Query Match	100.0%	Score 20; DB 6; Length 20;	PR	98113974-PI
Best Local Similarity	100.0%	Pred. No. 41;	PC	KARL HERMANN SCHLINGENSIEPEN, WOLFGANG PI
Matches	20;	Mismatches 0; Indels 0; Gaps 0;	PC	PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61P31/
Qy	1 GCTTTACCAAAATTGGAGC 20		PC	0, A61P5/00, A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A
Db			PH	method for stimulating the immune system
	1 GCTTTACCAAAATTGGAGC 20		FT	Location/Qualifiers
RESULT 3			FT	Source 1.. .20 /organism="Homo sapiens (human)".
BD065897	BD065897	20 bp DNA linear	FEATURES	Location/Qualifiers
LCUS		An antisense oligonucleotide preparation method.	source	1.. .20
DEFINITION				/organism="Homo sapiens"
ACCESSION	BD065897			/mol type="genomic DNA"
VERSION	BD065897			/db_xref="taxon:9606"
KEYWORDS	JP 200151100-A/532.		ORIGIN	
SOURCE	JP 200151100-A/532.		Query Match	100.0%; Score 20; DB 6; Length 20;
ORGANISM	unidentified		Best Local Similarity	100.0%; Pred. No. 41;
REFERENCE	unclassified.		Matches 20;	Mismatches 0; Indels 0; Gaps 0;
AUTHORS	1 (bases 1 to 20)		Qy	1 GCTTACCAAAATTGGAGC 20
TITLE	Schlingensiepen, K.H. and Brysch, W.		Db	1 GCTTACCAAAATTGGAGC 20
JOURNAL	An antisense Oligonucleotide Preparation method		FEATURES	
COMMENT	Patent: JP 200151100-A 532 07-AUG-2001;		source	1.. .20
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PN	JP 200151100-A/532			
PD	07-AUG-2001			
PP	30-JUN-1998 JP 19985322533			
PR	31-JUN-1997 EP 9701531-8			
PI	KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCHE			
PC	C12N15/11, C07H1/04, A61K31/70			
CC	An antisense oligonucleotide preparation method			
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DEFINITION	A method for stimulating the immune system.		Matches 20;	Mismatches 0; Indels 0; Gaps 0;
ACCESSION	BD234910		Qy	1 GCTTACCAAAATTGGAGC 20
VERSION	BD234910.1		Db	1 GCTTACCAAAATTGGAGC 20
KEYWORDS	JP 2002517434-A/14.			
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	RESULT 6			
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LOCUS	AX008981	Sequence 14 from Patent WO9963975.	20 bp	DNA	linear	PAT 06-SEP-2000	SOURCE	unidentified
DEFINITION	AK008981						ORGANISM	unclassified sequences.
VERSION	AX008981.1	GI:9996355					REFERENCE	1 (bases 1 to 18)
KEYWORDS	Homo sapiens (human)						AUTHORS	Brysch, W. and Schlingensiepen, K.
SOURCE	Homo sapiens						TITLE	AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.						JOURNAL	WO 9833904-A 1273 06-AUG-1998; BIOGNOSTIK GES (DE); BRYSCHE WOLFGANG (DE)
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REFERENCE	1	Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R.					source	1..18
AUTHORS								/organism="unidentified"
TITLE		A method for stimulating the immune system						/mol_type="unassigned DNA"
JOURNAL		Patent: WO 9963975-A 14 16-DEC-1999; BIONOSTIK GES (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REINAR (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REINAR (DE)						/db_xref="taxon:32644"
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Db							AUTHORS	Schlingensiepen, K.H. and Brysch, W.
ORIGIN							TITLE	An antisense oligonucleotide preparation method
Query Match		1 GCCTTCACCAATTGGAGC 20					JOURNAL	Patent: JP 2001511000-A 1273 07-AUG-2001; BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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Matches		Conservative 0; Mismatches 0; Indels 0; Gaps 0;					COMMENT	PN JP 2001511000-A/1273
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Db							COMMENT	PP 07-AUG-1998 JP 1998532533
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Matches		Conservative 0; Mismatches 0; Indels 0; Gaps 0;					COMMENT	FH Karl Hermann Schlingensiepen, Wolfgang Brysch
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Db							ACCESSION	BD234924
ORIGIN							VERSION	BD234924.1 GI:33044694
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Db							ACCESSION	BD234924
ORIGIN							VERSION	BD234924.1 GI:6737695
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ORIGIN							VERSION	BD234924.1 GI:33044694
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ORIGIN							VERSION	BD234924.1 GI:33044694
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Db							ACCESSION	BD234924
ORIGIN							VERSION	BD234924.1 GI:33044694
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Best Local Similarity		100.0%; Pred. No. 41;						
Matches								

RESULT 14
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 DEFINITION A method for stimulating the immune system.
 ACCESSION BD234926
 VERSION 1.1 GI:3304696
 KEYWORDS JP 2002517434-A/30.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
 TITLE A method for stimulating the immune system
 JOURNAL Patent: JP 2002517434-A 30 JUN 2002;
 COMMENT BIODIAGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
 OS Homo sapiens (human)
 PN JP 2002517434-A/30
 PD 18-JUN-2002
 PF 10-JUN-1999 JP 20000553044
 PR 10-JUN-1998 EP 98110709-7-25-JUL-1998 EP 98113974-4 PI
 KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
 BRYSCHE
 PC A61K45/06,A61K31/7088,A61K39/395,A61K39/395,A61P31/
 00,A61P35/00,
 PC A61P35/00,A61P37/02,C12N15/00,A61K37/02,C12N15/00 CC A
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 Db 1 TCACCAATTGGAGC 16

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 LOCUS Sequence 30 from Patent WO983975.
 DEFINITION Sequence 30 from Patent WO983975.
 ACCESSION AX008997
 VERSION AX008997.1 GI:9996371
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
 AUTHORS A method for stimulating the immune system
 TITLE Patent: WO 983975-A 30 16-DEC-1998;
 JOURNAL BIODIAGNOSTIK GES (DE); BRYSCHE WOLFGANG (DE); SCHLINGENSIEPEN REIMAR (DE); SCHLINGENSIEPEN KARL
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 ORIGIN

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OM nucleic - nucleic search, using bw model

Run on: March 4, 2006, 01:38:40 ; Search time 388.947 Seconds
(without alignments)
342.704 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: gctttcaccaaatttggaaatc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 499697 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4598950

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: genesegm1990s;*
3: genesegm2000s;*
4: genesegm2001as;*
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6: genesegm2002as;*
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12: genesegm2004ab;*
13: genesegm2004bs;*
14: genesegm2005s;*

SUMMARIES

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3	20	100.0	20	4	AAD18719	Human oil	AC	
4	18	90.0	18	3	AA265468	Immunosup	XX	
5	18	90.0	20	14	AB01191	TGF-beta	DT	
6	18	90.0	20	12	AD180035	Human tra	15-OCT-1998 (First entry)	
c	7	18	90.0	20	12	AD180181	Human tra	XX
8	16	80.0	16	3	AA265470	Immunosup	XX	
9	16	80.0	18	2	AAQ78430	TGF-beta	AAQ78430 TGF-beta	
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12	15	75.0	15	3	AA265469	Immunosup	AAZ65469 Immunosup	
c	13	14.2	71.0	20	12	ADP71056	Chicken 1	ADP71056 Mutant hu
c	14	14.2	71.0	20	12	ADK78529	Chimeric	ADK78529 Chimeric
c	15	14.2	71.0	20	12	ADK78529	Chimeric	ADK78529 Chimeric
c	16	14.2	71.0	24	6	AB225543	Human CD4	AB225543 Human CD4
c	17	14.2	71.0	32	2	AAV72954	Rat Munc1	AAV72954 Rat Munc1
c	18	14.2	71.0	40	12	ADP71056	Human Chk	ADP71056 Mutant hu
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ALIGNMENTS

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				XX	
				DT	
				15-OCT-1998 (First entry)	
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				DE	
					TGF-beta2 antisense oligonucleotide TGF-beta2-14.
				XX	
				XX	Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
				XX	modulate; gene expression; ss.
				XX	Synthetic.
				OS	Homo sapiens.
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				XX	
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				XX	
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				XX	97EP-00101531.
				PR	31-JAN-1997;
				XX	97EP-00101531.
				PA	(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
				XX	
				PI	Schillingensiepen K, Brysch W;
				XX	
				DR	WPI ; 1998-400910/35.
				XX	
				PT	Preparation of antisense oligo-nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture.
				PT	
				PT	
				PS	Claim 10: Fig 8a; 286pp; English.
				XX	
				CC	AAV48930-49007 represent antisense oligonucleotides directed against transforming growth factor-beta2 (TGF-beta2). Of these, only
				CC	Oligonucleotides AAV48930-67 resulted in significant reduction in TGF-beta 2 protein expression, while oligonucleotides AAV48968-49007 had

little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by $2R/3R = 0.33-0.72$. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, ErB-2, junB, junD, TGF-beta 1 or beta 2 to control proliferation of primary cells, osteoblasts (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or (activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.

that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the treatment of neoplasms and infections, particularly hyperproliferative; leukaemia, (non-Hodgkin's) lymphoma; carcinoma (of oesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas. The Oligonucleotides, most of which are directed against TGF β 2 or VEGF, are inhibitors of monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque.

```

Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
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      Best Local Similarity 100.0%; Pred. No. 4;3;
      Matches 20; Conservative 0; Mismatches 0; Indels 0;
      Gaps 0;

Query Match 100.0%; Score 20; DB 3; Length 20;
SQ      Best Local Similarity 100.0%; Pred. No. 4;3;
      Matches 20; Conservative 0; Mismatches 0; Indels 0;
      Gaps 0;

Qy 1 GCTTTACCAAAATGGAGC 20
Db 1 GCTTTACCAAAATGGAGC 20

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or cell expansion, where inhibition of tumour growth, improvement of organ or cell transplantation or cell expansion and enhancement or inhibition of immune response is enhanced in a supra-additive manner. The mixture is useful in drug target validation, i.e., to identify genes that are relevant for certain pathological state by testing the effect of the mixture on a cell system or organism. The present sequence is a human oligonucleotide useful in drug target validation

XX	Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;	Score 20; DB 4; Length 20;
Qy	Best local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Indels 0; Gaps 0	
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RESULT 4
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 XX
 AC
 KX
 DT
 XX
 08-SEP-2005 (first entry)
 TGF-beta 2 inhibition oligonucleotide SEQ ID NO 35.
 DDE
 XX
 pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
 Immunostimulant; Antiarthritic; Antirheumatic; Antiparisiatic;
 TGF-beta antagonist; Vaccine.

leukemias, acute or chronic myelocytic or lymphoblastic leukemia; tumor metastasis; benign tumors; or is chosen from bile carcinoma; bladder carcinoma; brain tumor; breast carcinoma; bronchogenic carcinoma; carcinoma of kidney; choriocarcinoma; cystadenocarcinoma; embryonal carcinoma; epithelial carcinoma; esophageal carcinoma; cervical carcinoma; colon carcinoma; colorectal carcinoma; endometrial carcinoma; gallbladder carcinoma; gastric carcinoma; head and neck carcinoma; liver carcinoma; lung carcinoma; mediastinal carcinoma; non-small cell carcinoma; bronchogenic/lung carcinoma; ovarian carcinoma; pancreas carcinoma; papillary carcinoma; papillary adenocarcinoma; prostate carcinoma; small intestine carcinoma; rectal carcinoma; renal cell carcinoma; skin carcinoma; small-cell bronchogenic/lung carcinoma; sonamogram; skin

carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence represents a TGF- β 2 inhibition oligonucleotide.

Sequence	20 BP;	6 A;	5 C;	4 G;	5 T;	0 U;	0 Other;
Query Match	100.0%;		Score 20;	DB 14;	Length 20;		
Best Local Matches	100.0%;		Pred. No. 4.3;				
Conservative	0;		Mismatches 0;				
			Indels 0;				
			Gaps 0;				
DY	1	GCCTTCACCAAATGGAGGC	20				
DB	1	GCCTTCACCAAATGGAGGC	20				

RESULT 5	
AAZ65468	AAZ65468 standard; DNA; 18 BP.
XX	AAZ65468;
AC	
XX	
DT	30-MAR-2000 (first entry)
XX	
DE	Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/1.
DE	Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW	vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW	prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW	monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
KW	Glomerulonephritis; acute respiratory distress syndrome; ss;
KW	atherosclerosis.
XX	

AC AAZ65453; DT 30-MAR-2000 (first entry) XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-13. XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGEx; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; OS Unidentified. XX OS Unidentified. XX PN WO9963975-A2. XX PD 16-DEC-1999. XX PP 10-JUN-1999; 99WO-EP004013. XX PR 10-JUN-1998; 98EP-00110709. XX PR 25-JUL-1998; 98EP-00113974. XX PA (BIOG-) BIODIAGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK. XX PI Schlingensiepen K, Schlingensiepen R, Brysch W; DR 2000-097470/08. XX PT Composition containing immune stimulant and inhibitor of agent that adversely affects the immune response, for treating cancers and infections. XX DR 2000-097470/08. XX PS Claim 5; Fig 1; 30pp; English.

This sequence is an immunosuppressant inhibitor oligonucleotide, which is used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor VEGF, interleukin-10 IL-10, prostaglandin E2 PGEx, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the treatment of neoplasms and infections, particularly hyperproliferation; leukaemia; (non-Hodgkin's) lymphoma, carcinoma (of oesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas; the oligonucleotides, most of which are directed against TGFbeta or VEGF, are inhibitors of monocyte chemotactic protein-1 (MCP-1) and are useful as anti-inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque

Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match Score 16; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX SQ

5 TCACCAATTGGAAAGC 20
1 TCACCAATTGGAAAGC 16

Query Match Score 16; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX SQ

5 TCACCAATTGGAAAGC 20
1 TCACCAATTGGAAAGC 16

RESULT 11
AAB01190 ID AAZ65459 AC AAZ65469; XX DR 30-MAR-2000 (first entry) XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/2. XX AC AAZ65469;

DT 08-SEP-2005 (first entry) XX TGF-beta 2 inhibition oligonucleotide SEQ ID NO 34. XX Pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic; Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic; TGF-beta antagonist; Vaccine. XX Synthetic. OS XX WO2005059133-A2. XX PD 30-JUN-2005. XX XX 20-DEC-2004; 2004WO-EP053604. XX PR 19-DEC-2003; 2003EP-00029367. XX PR 05-FEB-2004; 2004US-0541771P. XX (ANTI-) ANTISENSE PHARMA GMBH. XX PI Schlingensiepen K, Schlingensiepen R; DR 2005-479334/48. XX PT Pharmaceutical composition useful for treating neoplaam, comprises PT stimulators stimulating function of immune system and/or immune cells and substances inhibiting cell proliferation and/or inducing cell death. XX PS Claim 4; SEQ ID NO 34; 46pp; English.

The invention relates to a pharmaceutical composition (PC) comprising one or more substances inhibiting cell proliferation and/or CC immune cells and one or more substances that stimulate the function of immune system and/or CC or more stimulators that stimulate the function of immune system and/or CC and/or inducing cell death. A pharmaceutical composition is useful for creating neoplasms chosen from solid tumors; tumor CC leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma, carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal carcinoma, epithelial carcinoma, esophageal carcinoma, cervical carcinoma, epidermal carcinoma, colorectal carcinoma, endometrial carcinoma, gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell CC carcinoma, papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, small intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence represents a TGF-beta 2 inhibition oligonucleotide.

Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match Score 16; DB 14; Length 18; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX SQ

5 TCACCAATTGGAAAGC 20
1 TCACCAATTGGAAAGC 16

RESULT 12
AAB01190 ID AAZ65469 AC AAZ65469; XX DR 30-MAR-2000 (first entry) XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/2. XX AC AAZ65469;

Immunosuppressive inhibitor, transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss; atherosclerosis.

XX OS Unidentified.

XX WO9963975-A2.

XX I6-DECPD 16-DEC-1999.

XX 10-JUN-1999; 99WO-EPO04013.

XX 10-JUN-1998; 98EP-00110709.

XX 25-JUL-1998; 98EP-00113974.

(BIOG-) BIODIAGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PA Schlingensiepen K, Schlingensiepen R, Brysch W;

XX PPA WPP; 2000-097470/08.

XX PPT Composition containing immune stimulant and inhibitor of agent that adversely affects the immune response, for treating cancers and infections.

XX PPT Claim 5; Fig 1; 30PP; English.

XX PPT This sequence is an immunosuppressant inhibitor oligonucleotide, which is used in the invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor VEGF, interleukin-10 IL-10, prostaglandin E2 PGF2, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the treatment of neoplasms and infections, particularly hyperproliferation; leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas. The oligonucleotides, most of which are directed against TGFbeta or VEGF, are inhibitors of monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-inflammatory agents for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque.

XX Gallus sp.
 XX OS
 XX WO200279447-A2.
 XX PN
 XX PD 10-OCT-2002.
 XX PF 29-MAR-2002; 2002WO-US009866.
 XX PR 30-MAR-2001; 2001US-0280004P.
 XX PR 03-AUG-2001; 2001US-00922549.
 XX PR 25-JAN-2002; 2002US-0351550P.
 XX PA (AVIG-) AVIGENICS INC.
 XX PA (AVIG-) AVIGENICS INC.
 PI Rapp JC;
 XX DR WPI; 2003-046807/04.
 XX PT New isolated or recombinant nucleic acid for reducing the chromosomal
 PT positional effect of a transgene, comprises an isolated avian lysozyme
 PT gene expression control region.
 XX PS Example 1; Fig 1; 88pp; English.
 XX CC The invention relates to an isolated or recombinant nucleic acid or DNA
 CC molecule comprising an isolated avian lysozyme gene expression control
 CC region operably linked to a nucleic acid insert encoding a polypeptide.
 CC The nucleic acid is useful for reducing the chromosomal positional effect
 CC of a transgene operably linked to the lysozyme gene expression control
 CC region and transfected into a recipient avian cell. The present sequence
 CC is a PCR primer used for sequencing chicken lysozyme gene expression
 CC control region
 XX SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
 XX Query_Match 71.0%; Score 14.2; DB 8; Length 20;
 XX Best_Local_Similarity 84.2%; Pred. No. 3.ee+03;
 XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GCTTACCAAAATTGGAG 19
 Db 20 GCTGACCAACATGGAG 2
 XX RESULT 14
 ADK78448/C
 ID ADK78448 standard; DNA; 20 BP.
 XX AC ADK78448;
 XX DT 20-MAY-2004 (First entry)
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5782.
 XX KW Nav1.3; Analgesics; Nootropic; Neuroprotective; post-herpetic neuralgia;
 KW diabetic neuropathy; arthritic pain; migraine headache;
 KW infantile epilepsy; ataxia; ss.
 XX OS Synthetic.
 XX PN WO2004016754-A2.
 XX PD 26-FEBB-2004.
 XX PR 14-AUG-2003; 2003WO-US025165.
 XX PR 14-AUG-2002; 2002US-0403416P.
 XX PA (PHAA) PHARMACIA CORP.
 XX PI Roberts SL;

WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding Nav1.3; useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.

XX Claim 4; SEQ ID NO 5782; 417pp; English.

XX The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.

XX The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy, or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

SQ Query Match 71.0%; Score 14.2%; DB 12; Length 20;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTTTACCAATTGGAG 19
Db 19 GCTTCCACCAATGGAG 1

RESULT 15

ADK78529/C
ID ADK78529 Standard; DNA; 20 BP.
XX AC ADK78529;

XX DT 20-MAY-2004 (First entry)

XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5863.
XX KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX OS Synthetic.
XX PN WO2004016754-A2.
XX PD 26-FEB-2004.
XX PF 14-AUG-2003; 2003WO-US025465.

XX PR 14-AUG-2002; 2002US-0403416P.
XX PA (PHAA) PHARMACIA CORP.
XX PI Roberds SL;
XX DR WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding Nav1.3; useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.

XX Claim 4; SEQ ID NO 5863; 417pp; English.

XX The present invention relates to an antisense compound targeted to a

CC nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy, or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target different regions of the human Nav1.3 RNA.

SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2%; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTTCACCAATTGGAG 19

Db 20 GCTTCCACCAATGGAG 2

Search completed: March 4, 2006, 02:31:42
Job time : 393.947 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	BH905278	BH905278
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	AZ864054	2M0173M19
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	BH903531	BH91028
	AU259281	AU259281
	BH856768	SALK_0791
	AJ596091	Arabidopsis
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	CZ471273	C07136-3P
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	AZ658401	1M0535M17
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post-processing: Minimum Match 0% Maximum Match 100%

RESULT 1	EST:*	34 bp	mRNA	linear	EST 08-NOV-2001
LOCUS	AV852639	34 bp	mRNA	linear	EST 08-NOV-2001
DEFINITION	AV852639 Nori Satoh unpublished cDNA library, larva Ciona intestinalis cDNA clone rc1iv19c08 3', mRNA sequence.	34 bp	mRNA	linear	EST 08-NOV-2001
ACCESSION	AV852639	34 bp	mRNA	linear	EST 08-NOV-2001
VERSION	AV852639.1	34 bp	mRNA	linear	EST 08-NOV-2001
KEYWORDS	EST.	34 bp	mRNA	linear	EST 08-NOV-2001
SOURCE	Ciona intestinalis	34 bp	mRNA	linear	EST 08-NOV-2001
ORGANISM	Ciona intestinalis	34 bp	mRNA	linear	EST 08-NOV-2001
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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

MARTES

Result No.	Score	Query Match	Length	DB ID	Description	FEATURES source	FEATURES source	FEATURES source	ORIGIN
1	13.4	67.0	34	1 AV852639	AV852639 CGT29682 1119111B0				
2	12.8	64.0	25	10 CGT29682	A1034270	/organism="Ciona intestinalis" /mol type="mRNA"			
3	12.8	64.0	31	1 BZ769257	BZ769257 SALK_1418	/db_xref="taxon:7719"			
4	12.6	63.0	33	9 A2336391	A2336391 IMO766G07	/clone="rc1v19c08"			
5	12.4	62.0	35	9 BH863411	BH863411 SALK_0938	/tissue_type="whole animal"			
6	12.2	61.0	34	9 AZ645914	AZ645914 IMO511K08	/dev_stage="larva"			
7	12.2	61.0	34	9 AZ308115	AZ308115 IMO010J17	/clone_lib="Nor1 Satoh unpublished cDNA library, larva"			
8	12	60.0	21	9					
9	12	60.0	27	10 AG204809	AG204809 Pan trogl				
10	12	60.0	32	9 BH904979	BH904979 SALK_1054				
11	12	60.0	32	10 AJ600156	AJ600156 Arabidops				
12	11.8	59.0	31	5 BQ587054	AU255583 AU255583				
13	11.8	59.0	32	5 BZ661352	BQ887054 B012351-0				
14	11.8	59.0	36	9 BZ661352	BZ661352 SALK_0248				
15	11.8	59.0	37	1 AA887375	AA1823627 w155_028				
16	11.8	59.0	40	1 AA887375	AA887375 oj13908_S				
17	11.8	59.0	40	1 AA961031	AA961031 op08911_S				
18	11.6	58.0	31	1 CR395105	CR395105 Arabidops				
19	11.6	58.0	34	9 A2789746	A2789746 2M00037M14				
20	11.6	58.0	34	11 CR358544	CR358544 Arabidops				
21	11.6	58.0	35	9 BH854633	BH854633 KG08875-5				
22	11.4	57.0	19	1 AT790036	AT790036 KEG6811_L				
					CG29682/c				
					RESULT 2				

LOCUS	CG79682	25 bp	DNA	linear	GSS 20-OCT-2003	REFERENCE	1 (bases 1 to 31)	
DEFINITION	1119114B03..28L_Y1_1119 - Rescuemu Grid AA Zea mays genomic, genomic survey sequence.					AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
ACCESSION	CG79682					TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
KEYWORDS						JOURNAL	Unpublished (1997)	
SOURCE	GSS.					COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapsbs@mail.nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.	
ORGANISM	Zea mays						cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINN at: www-bio.llnl.gov/bbrp/image/image.html	
REFERENCE	Bukar-Yote, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.							
AUTHORS	Walbot, V.							
TITLE	Maize genomic sequences found using engineered Rescuemu transposon							
JOURNAL	Unpublished (2001)							
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 155 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu							
FEATURES	Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 119114 row: B column: 03					FEATURES	source	
Source						source	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1646533" /issue_type="parathyroid tumor" /dev_stage="adult" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares_Parathyroid tumor_NbHPA" /note="Organ: parathyroid gland; Vector: pPTT3D (Pharmacia) with a modified polylinker Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTACCAANTGAAAGTGGAGGCCGACCAATTTTTTTTTTTTTTT-3'] , double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pPTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bent Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."	
Location/Qualifiers						ORIGIN		
1..25						Query Match	64.0% Score 12.8; DB 1; Length 31;	
						Best Local Similarity	87.5%; Pred. No. 1.6e+05;	
						Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
						Qy	3 TTTCACCAAATGGAA 18	
						Db	19 TTCCAGCRAATGGAA 4	
FEATURES						RESULT	4	
Source						ACCESSION	BZ769257/C	
						VERSION	BZ769257.1	
						KEYWORDS	GSS.	
						DEFINITION	SALK_141059..37.05.x Arabidopsis thaliana TUNA insertion lines	
						ORGANISM	Arabidopsis thaliana genomic clone SALK_141059..37.05.x, genomic survey sequence.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					REFERENCE	RESULTS	
REFERENCE	AI034270	31 bp	mRNA	linear	EST 25-JUN-1998	AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,	
ACCESSION	AI034270..x1	Soares_Parathyroid tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1646933..3', similar to TR:P97536 P97536 TIP120..;, mRNA sequence.				TITLE	Gadrinab,C., Jeske,A., Kernes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.	
VERSION	AI034270						A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome	
KEYWORDS	Homo sapiens (human)							
SOURCE	Homo sapiens							
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							

JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 1001 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g35820.

FEATURES source

Location/Qualifiers 1..33
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
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 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query	Match	Score	Length	DB	9%	Score	Length	DB	9%
Qy	1 GCTTACCAATTGGAG 19	63.01	33;	62.4	35;	2 CTTTCACCAATTG 15	62.0%	35;	12.4
Db	32 GCTTACCAAGTTGTAG 14	Pred. No. 2e+05;	Indels 0;	Mismatches 0;	Conservative 0;	Indels 1;	Mismatches 1;	Conservative 0;	Indels 0;

RESULTS 5

LOCUS	DEFINITION	ACCESION	KEYWORDS	SOURCE	ORGANISM	COMMENT
AZ336391	IM0066G07R Mouse 10kb plasmid UUGCIM0066G07 R, genomic survey sequence.	AZ336391.1	GI:10405642	Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciuromorphata; Muroidea; Muridae; Murinae; Mus.	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dduann@genetics.utah.edu Insert Length: 10000 Std Error: 0.00
				Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Imlay,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhauern,A. and Wright,D., Waiss,R.	REFERENCE AUTHORS	Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhauern,A. and Wright,D., Waiss,R.
				Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
				Unpublished (2000)	JOURNAL	Arabidopsis thaliana (thale cress)
				Contact: Robert B. Weiss	COMMENT	Arabidopsis thaliana
				Email: dduann@genetics.utah.edu		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eu dicotyledons; rosids; eu rosids II; Brassicales; Brassicaceae; Arabidopsis.
				Insert Length: 10000 Std Error: 0.00		Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrab,C., Jeste,A., Karres,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
				Plate: 0066 row: G column: 07		REFERENCE
				Seq primer: CACACGAAACAGCTATGACC		1..26 (bases 1 to 35)
				Class: Plasmid ends		(bases 1 to 26)
				High quality sequence stop: 35.		
				Location/Qualifiers 1..35		
				/organism="Mus musculus"		

FEATURES source

/clone="SALK 093836"
/CloneLib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at <http://signal.salk.edu/tdna/protocols.html>"

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732119b|AF129022.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL1-Gold "Stratagene" cells and selected for ampicillin resistance.

ORIGIN

Query	Match	Score 12.2;	DB 9;	Length 34;
	Best Local Similarity	61.0%;	Score 12.2;	DB 9;
	Matches	82.4%;	Pred. No. 3.1e+05;	Length 34;
	Matches	14;	Conservative	Prod. No. 3.2e+05;
		0;	0;	Mismatches 0;
		Indels 3;	Indels 3;	Indels 0;
		Gaps 0;	Gaps 0;	Gaps 0;

and selected for ampicillin resistance."

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114 9b AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CTTCACCAAT 13
Db 20 CTTCACCAAT 9

RESULT 9
AG204809/c
LOCUS AG204809 27 bp DNA, clone: RP43-090L01.T7, genomic survey sequence.
DEFINITION AG204809_1 GI:45236984
ACCESSION AG204809
VERSION GSS
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Pan troglodytes
ORGANISM Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.

REFERENCE Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Yun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
AUTHORS BAC end sequences of Library RP-43
JOURNAL Unpublished
PRIMERS Sequencing: T7

REFERRALS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Yun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail: fedstone@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/, Tel: 82-42-66-7181, Fax: 82-42-860-4409)

COMMENT Clones were derived from the chimpanzee BAC library RP-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

LIBRARY Vector : pBCE3.6
R.Site 1 : Ecoli
R.Site 2 : Ecoli
FEATURES Source 1..27
/organism="Pan troglodytes"
/mol_type="Genomic DNA"
/db_xref="taxon:9599"
/sex="male"
/cell_type="lymphocytes"
/clone_id="RP43-090L01.T7"

ORIGIN Query Match 60.0%; Score 12; DB 10; Length 27;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 26 GGTTTACCCAGATTAAATGC 7

RESULT 1.0
BH904979/c
LOCUS BH904979 32 bp DNA linear GSS 04-SEP-2002
DEFINITION SALK 105414-53.00 x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_105414.53.00.x, Genomic survey sequence.

ACCESSION BH904979
VERSION BH904979.1 GI:22717726
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 32)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gaddinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
AUTHORS A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
TITLE Unpublished (2001)
JOURNAL Contact: Joseph R. Ecker
COMMENT Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of TDNA. At g901820. Class: TDNA tagged.

FEATURES Source 1..32
/organism="Arabidopsis thaliana"
/mol_type="Genomic DNA"
/eco_type="Col-0"
/db_xref="taxon:3702"
/clone="SALK_105414-53.00.x"
/clone_id="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html"

ORIGIN Query Match 60.0%; Score 12; DB 9; Length 32;
Best Local Similarity 75.0%; Pred. No. 4e+05; Matches 15; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTACCAATTGGAAAGC 20
Db 31 GCTTACATAATTGAAAC 12

RESULT 1.1
AJ600156
LOCUS AJ600156 32 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 501c03, genomic survey sequence.

ACCESSION AJ600156.1 GI:37949784
VERSION AJ600156
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Qy 1 GCCTTCACCAATTGGAAAGC 20

REFERENCE	1	AUTHORS	Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Craud,C., Derose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lechatnay,A.	JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)	PUBLMED	12446565	REFERENCE	2 (bases 1 to 32)
AUTHORS	Balzergue,S.	TITLE	Direct Submission	COMMENT	Submitted (23-OCT-2003) Balzergue S., INRA/CNRS, 2 rue Gaston Crémieux, 91057 Evry cedex, FRANCE	PCR was performed on DNA from transformants of <i>Arabidopsis thaliana</i> plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).	FEATURES	Source	
FEATURES	misc_feature	ORIGIN	Query Match	Best Local Similarity	Score 12; DB 10; Length 32;	Match	1 GCTTTCACCAATTGGAAAGC 20		
FEATURES	source	ORIGIN	Query Match	Best Local Similarity	Score 12; DB 10; Length 32;	Match	1 GCTTTCACCACTGTGGAGC 20		
REFERENCE	RESULT 12	LOCUS	AU255583	DEFINITION	31 bp mRNA linear EST 25-APR-2002	VERSION	BE00005815 3', mRNA sequence.		
REFERENCE	AU255583/c	KEYWORDS	AU255583	ACCESSION	Mus musculus (house mouse)	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchoptoglires; Glires; Rodentia; Mus. Sciurognathi; Murioidea; Muridae; Murinae; Mus. 1 (bases 1 to 31)		
REFERENCE	AU255583/c	AUTHORS	Kato,K. and Matoba,P.	JOURNAL	Generation of expressed sequence tags from mouse brain	COMMENT	Contact: Kikuya Kato		
REFERENCE	AU255583/c	AUTHORS	Graduate School of Biological Sciences	JOURNAL	Nara Institute of Science and Technology	COMMENT	891-5 Takayama, Ikoma, Nara 630-0101, Japan		
REFERENCE	AU255583/c	AUTHORS	TEL: 81-743-72-5581	JOURNAL	FAX: 81-743-72-5589	COMMENT	Email: kikato@bs.aist-nara.ac.jp ,		
FEATURES	AU255583/c	URL: http://loren2.aist-nara.ac.jp/BED/index.html .							

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OM nucleic - nucleic search, using bw model

Run on: March 4, 2006, 01:49:32 ; Search time 76.8421 Seconds
(without alignments)
462.653 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gctttcaccaaatttggaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88780828 residues

Total number of hits satisfying chosen parameters: 1198766

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database	Issued_Patents_NA:
	1: /cgn2_6_ptodata/1/ina/1_COMB.seq:*
	2: /cgn2_6_ptodata/1/ina/5_COMB.seq:*
	3: /cgn2_6_ptodata/1/ina/6A_COMB.seq:*
	4: /cgn2_6_ptodata/1/ina/6B_COMB.seq:*
	5: /cgn2_6_ptodata/1/ina/H_COMB.seq:*
	6: /cgn2_6_ptodata/1/ina/P_COMB.seq:*
	7: /cgn2_6_ptodata/1/ina/PP_COMB.seq:*
	8: /cgn2_6_ptodata/1/ina/RE_COMB.seq:*
	9: /cgn2_6_ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	16	80.0	18	3	US-09-535-249-79	Sequence 79, Appl
2	14.2	71.0	25	3	US-09-396-196G-6827	Sequence 6827, Appl
c 3	13.8	69.0	29	3	US-09-304-232-470	Sequence 470, Appl
4	13.2	66.0	24	2	US-08-467-590-42	Sequence 42, Appl
5	13.2	66.0	24	3	US-08-711-417C-42	Sequence 42, Appl
6	13.2	66.0	24	3	US-09-723-909-42	Sequence 42, Appl
7	13.2	66.0	24	6	PCT-US93-08743-42	Sequence 1227784, Appl
8	13.2	66.0	25	3	US-09-396-196G-122784	Sequence 1227784, Appl
c 9	12.8	64.0	19	3	US-09-691-4062	Sequence 4062, Appl
c 10	12.8	64.0	25	3	US-09-690-791-4063	Sequence 4063, Appl
c 11	12.8	64.0	25	3	US-09-396-196G-71637	Sequence 71637, Appl
c 12	12.8	64.0	25	3	US-09-396-196G-71638	Sequence 71638, Appl
c 13	12.8	64.0	25	3	US-09-396-196G-71639	Sequence 71639, Appl
c 14	12.8	64.0	25	3	US-09-396-196G-71640	Sequence 71640, Appl
c 15	12.8	64.0	25	3	US-09-396-196G-71641	Sequence 71641, Appl
c 16	12.8	64.0	25	3	US-09-396-196G-71642	Sequence 71642, Appl
c 17	12.8	64.0	26	2	US-08-118-387-4	Sequence 4, Appl
c 18	12.8	64.0	29	2	US-08-304-871-39	Sequence 39, Appl
c 19	12.8	64.0	30	3	US-08-567-959-39	Sequence 12, Appl
c 20	12.8	64.0	30	3	US-08-541-381B-137	Sequence 137, Appl
c 21	12.6	63.0	21	2	US-08-81-806-12	Sequence 12, Appl
c 22	12.6	63.0	21	3	US-09-293-854-12	Sequence 12, Appl
c 23	12.6	63.0	25	3	US-09-396-196G-16724	Sequence 16724, Appl
c 24	12.6	63.0	25	3	US-09-396-196G-18361	Sequence 18361, Appl

ALIGNMENTS

RESULT 1
US-08-535-249-79
Sequence 79, Application US/08535249
Patent No. 6155689

GENERAL INFORMATION:
 APPLICANT: Schlingensiepen, Georg-Ferdinand
 APPLICANT: Brysch, Wolfgang
 APPLICANT: Karl-Hermann
 APPLICANT: Schlingensiepen, Reimar
 APPLICANT: Bogdahn, Ulrich
 TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
 NUMBER OF SEQUENCES: 137

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jacobson, Price, Holman & Stern
 STREET: 400 Seventh St. N.W.
 CITY: Washington D.C.
 COUNTRY: U.S.A.
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,249
 FILING DATE:
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP 93 107 083.0
 FILING DATE: 30-APR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP 93 107 849.7
 FILING DATE: 13-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Player, William E.
 REGISTRATION NUMBER: 31,409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)338-6666
 TELEX: (202)395-3350
 INFORMATION FOR SEQ ID NO: 79:
 SEQ ID: RCA 248593 IDEA UR
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown

TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 ANTI-SENSE: YES
 US-08-535-249-79

Query Match Score 16; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCAACCAATTGGAGC 20
 Db 1 TCAACCAATTGGAGC 16

RESULT 2
 US-09-396-196G-6627
 Sequence 6827, Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 APPLICANT: David Mack
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: US/09/396.196G
 PRIORITY NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6827
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-396-196G-6627

Query Match Score 14.2%; DB 3; Length 25;
 Best Local Similarity 84.2%; Pred. No. 5.6e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CTTTCACCAATTGGAGC 20
 Db 5 CTTCAGCAAGTAGAACG 23

RESULT 3
 US-09-104-232-470/C
 Sequence 470, Application US/09304232
 Patent No. 6525185
 GENERAL INFORMATION:
 APPLICANT: Pan, Jian Bing
 APPLICANT: Chakravarti, Aravinda
 APPLICANT: Halushka, Marc Kenneth
 APPLICANT: Case Western Reserve University School of Medicine
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Polymorphisms Associated With Hypertension
 FILE REFERENCE: 018547-034210US
 CURRENT APPLICATION NUMBER: US/09/304,232
 CURRENT FILING DATE: 1999-05-03
 EARLIER APPLICATION NUMBER: US 60/084,641
 EARLIER FILING DATE: 1998-05-07
 NUMBER OF SEQ ID NOS: 909
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 470
 LENGTH: 29
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: GH2EX3 126
 US-09-304-232-470

Query Match Score 13.8%; DB 3; Length 29;
 Best Local Similarity 78.9%; Pred. No. 9.2e+02;
 Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCCTTCACCAATTGGAG 19
 Db 25 GTTTCACCCMGTGGAG 7

RESULT 4
 US-08-465-590-42
 Sequence 42, Application US/08465590
 Patent No. 5824770
 GENERAL INFORMATION:
 APPLICANT: Georgopoulos, Katia A.
 TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
 NUMBER OF SEQUENCES: 164
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 STATE STREET, Suite 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,590
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/238,212
 FILING DATE: 02-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/121,438
 FILING DATE: 14-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/946,233
 FILING DATE: 14-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Paul L.
 REGISTRATION NUMBER: 35,695
 REFERENCE DOCKET NUMBER: MPG-006G2DV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-465-590-42

Query Match Score 13.2%; DB 2; Length 24;
 Best Local Similarity 83.3%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TTTCACCAATTGGAGC 20
 Db 5 TTAAACCAATTGGAGC 22

RESULT 5
 US-08-711-417C-42
 Sequence 42, Application US/08711417C
 Patent No. 6228611
 GENERAL INFORMATION:
 TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 202
 CORRESPONDENCE ADDRESS: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:

DISKETTE

IBM COMPATIBLE

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/711,417C

FILING DATE: 05-SEP-1996

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/238,212

FILING DATE: 02-MAY-1994

APPLICATION NUMBER: 08/121,438

FILING DATE: 14-SEP-1993

APPLICATION NUMBER: 07/946,233

FILING DATE: 14-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis P.

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10287/007001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-08-711-17C-42

Query Match

66.0%;

Score 13.2;

DB 3;

Length 24;

Pred. No. 1.8e+03;

Matches 15;

Conservative

0;

Indels 0;

Gaps 0;

;

Qy 3 TTTCACCAATTGGAGC 20

5 TTTAACCAATTGGAGC 22

Db

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RESULT 6

us-09-723-909-42

Sequence 42, Application US/09723909

Patent No. 6630141

GENERAL INFORMATION:

APPLICANT: Georgopoulos, Katia A.

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 202

CORRESPONDENCE ADDRESS:

ADDRESSE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

DISKETTE

IBM COMPATIBLE

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/723,909

FILING DATE: 28-No. 6630141-2000

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/711,417

FILING DATE: 05-SEP-1996

APPLICATION NUMBER: 08/238,212

FILING DATE: 02-MAY-1994

APPLICATION NUMBER: 08/121,438

FILING DATE: 14-SEP-1993

APPLICATION NUMBER: 07/946,233

FILING DATE: 14-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis P.

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10287/007001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-09-723-909-42

Query Match

66.0%;

Score 13.2;

DB 3;

Length 24;

Pred. No. 1.8e+03;

Matches 15;

Conservative

0;

Indels 0;

Gaps 0;

;

Qy 3 TTTCACCAATTGGAGC 20

5 TTTAACCAATTGGAGC 22

Db

;

RESULT 7

PCT-US93-08743-42

; Sequence 42, Application PC/TUS93/08743

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 152

COMPUTER READABLE FORM:

DISKETTE

IBM PC compatible

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08743

PRIOR APPLICATION DATA:

PCT-US93-08743-42

; Sequence 42, Application PC/TUS93/08743

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 152

COMPUTER READABLE FORM:

DISKETTE

IBM PC compatible

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08743

PRIOR APPLICATION DATA:

PCT-US93-08743-42

; Sequence 42, Application PC/TUS93/08743

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 152

COMPUTER READABLE FORM:

DISKETTE

IBM COMPATIBLE

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/723,909

FILING DATE: 28-No. 6630141-2000

RESULT 8
US-09-396-196G-122784
Sequence 122784, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-08-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 122784
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-122784

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TTTTACCAATTGGAAGC 20
Db 4 TTTCATCTAACATGGAGC 21

RESULT 9
US-09-596-791-4062/c
Sequence 4062, Application US/09696791
Patent No. 6770633
GENERAL INFORMATION
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: SKIN AND EYE DISEASES
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4062
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-596-791-4062

Query Match 64.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTTTACCAATTGGA 17
Db 19 CCTTAAACAAATTGGA 4

RESULT 10
US-09-596-791-4063/c
Sequence 4063, Application US/09696791
Patent No. 6770633
GENERAL INFORMATION
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EYE DISEASES

RESULT 11
US-09-396-196G-71637
Sequence 71637, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
PRIORITY NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71637
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-71637

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCTTACCAATTGGA 16
Db 10 GCTGTCAACCATTGGA 25

RESULT 12
US-09-396-196G-71638
Sequence 71638, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
PRIORITY NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71638
LENGTH: 25

```

; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71638

Query Match Score 64.0%; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCTTTCACCAATGG 16
Db 8 GCTGTACCAATTTGG 23

RESULT 13
US-09-396-196G-71639
Sequence 71639, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
PRIORITY FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71641
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-71639

Query Match Score 64.0%; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCTTTCACCAATGG 16
Db 7 GCTGTACCAATTTGG 22

RESULT 14
US-09-396-196G-71640
Sequence 71640, Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
PRIORITY FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71640
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-71640

Query Match Score 64.0%; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCTTTCACCAATGG 16
Db 4 GCTGTACCAATTTGG 19

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NUMBER OF SEQ ID NOS: 673904
SEQ ID NO: 447577
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-447577

Query Match 76.0% Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 20 GCTTTCACCAATTGGAGC 20
Db 20 GCTTTCACCAATTGGAGC 1

RESULT 3
US-11-136-527-278180
Sequence 278180, Application US/11136527
Publication No. US2005028757041
GENERAL INFORMATION:
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136.527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SEQ ID NO: 278180
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Probe
US-11-136-527-278180

Query Match 76.0% Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 1 GCTTTCACCAATTGGAGC 20
Db 3 GCTTTCAGCTAAATTGGAGTC 22

RESULT 4
US-11-121-849-634116/C
Sequence 634116, Application US/11121849
Publication No. US2005027208041
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 634116
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-634116

Query Match 75.0% Score 15; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 3 TTTACCCAAATTGGA 17
Db 15 TTTCACCAATTGGA 1

RESULT 5
US-11-121-849-583444
Sequence 583444, Application US/11121849
Publication No. US2005027208041
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 583444
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-583444

Query Match 74.0% Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 3 TTTACCCAAATTGGAAGC 20
Db 6 TTCCACCAAATGGAAAGC 23

RESULT 6
US-10-310-914A-323453
Sequence 323453, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bantwich, Isaac
APPLICANT: Shuler, Krutzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.020.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO: 323453
LENGTH: 24
TYPE: RNA
ORGANISM: Human
US-10-310-914A-323453

Query Match 72.0% Score 14.4; DB 8; Length 24;
Best Local Similarity 62.5%; Pred. No. 9.7e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 1 GCTTTCACCAATTGG 16
Db 4 GCTUCACCAAUAGG 19

RESULT 7
US-11-121-849-206297/C
Sequence 206297, Application US/11121849
Publication No. US2005027208041
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 634116
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-634116

Query Match 75.0% Score 15; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 3 TTTACCCAAATTGGA 17
Db 15 TTTCACCAATTGGA 1

```

```

FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIORITY FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 206297
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
us-11-121-849-206297

Query Match    72.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TTTCACCAATTGGAA 18
Db      17 TTTCACCAATTAGGAA 2

RESULT 10
US-11-121-849-206857/c
; Sequence 206857, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;   APPLICANT: John Palma
;   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sequences
;   FILE REFERENCE: 3684.1
;   CURRENT APPLICATION NUMBER: US/11/121,849
;   CURRENT FILING DATE: 2005-05-03
;   PRIOR APPLICATION NUMBER: 60/567,949
;   PRIOR FILING DATE: 2004-05-03
;   NUMBER OF SEQ ID NOS: 673904
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;   SEQ ID NO: 206857
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
us-11-121-849-206857

Query Match    72.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TTTCACCAATTGGAA 18
Db      16 TTTCACCAATTAGGAA 1

RESULT 8
US-11-121-849-206298/c
; Sequence 206298, Application US/11121849
; Publication No. US/20050272080A1
; GENERAL INFORMATION:
;   APPLICANT: John Palma
;   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sequences
;   FILE REFERENCE: 3684.1
;   CURRENT APPLICATION NUMBER: US/11/121,849
;   CURRENT FILING DATE: 2005-05-03
;   PRIOR APPLICATION NUMBER: 60/567,949
;   PRIOR FILING DATE: 2004-05-03
;   NUMBER OF SEQ ID NOS: 673904
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;   SEQ ID NO: 206298
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
us-11-121-849-206298

Query Match    72.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TTTCACCAATTGGAA 18
Db      16 TTTCACCAATTAGGAA 1

RESULT 11
US-10-310-914A-1191627
; Sequence 1191627, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
;   APPLICANT: Bentwich, Isaac
;   TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and their uses thereof
;   FILE REFERENCE: 06087.0200.CPUS01
;   CURRENT APPLICATION NUMBER: US/10/310,914A
;   CURRENT FILING DATE: 2002-12-06
;   NUMBER OF SEQ ID NOS: 1388102
;   SOFTWARE: PatentIn version 3.3
;   SEQ ID NO: 1191627
;   LENGTH: 25
;   TYPE: RNA
;   ORGANISM: Human
us-10-310-914A-1191627

Query Match    71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 68.4%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CTTTCACCAATTGGAGC 20
Db      6 cuucaccacatggagc 24

RESULT 12
US-11-121-849-191
; Sequence 191, Application US/11121849
; Publication No. US/20050272080A1
; GENERAL INFORMATION:
;   APPLICANT: John Palma
;   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sequences
;   FILE REFERENCE: 3684.1
;   CURRENT APPLICATION NUMBER: US/11/121,849
;   CURRENT FILING DATE: 2005-05-03
;   PRIOR APPLICATION NUMBER: 60/567,949
;   PRIOR FILING DATE: 2004-05-03
;   NUMBER OF SEQ ID NOS: 673904
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;   SEQ ID NO: 206856
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
us-11-121-849-206856

```

```

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded DNA Sequencing Using Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIORITY FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 191
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-191

Query Match 71.0%; Score 14.2%; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CTTTCACCAAAATTGGAAGC 20
Db 4 CATGACCTAATGGAAAC 22

RESULT 13
US-11-121-849-345854
Sequence 345854, Application US/11121849
; GENERAL INFORMATION
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded DNA Sequencing Using Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIORITY FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 345854
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-345854

Query Match 71.0%; Score 14.2%; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CTTTCACCAAAATTGGAAGC 20
Db 2 CCTTGACCAAAATGGAAAC 20

RESULT 14
US-11-121-849-673774
Sequence 673774, Application US/11121849
; GENERAL INFORMATION
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded DNA Sequencing Using Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIORITY FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 673774
; LENGTH: 25
; TYPE: DNA

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OM nucleic - nucleic search, using bw model

Run on: March 4, 2006, 01:49:48 ; Search time 417.368 Seconds

(without alignments)
396.263 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gctttcaccaaatttggaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:

10900902

Minimum DB seq length: 0

Maximum DB seq length: 540

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:
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 2: /cgn2_6/ptodata/1/pubnra/US08_PUBCOMB.seq/*
 3: /cgn2_6/ptodata/1/pubnra/US09A_PUBCOMB.seq/*
 4: /cgn2_6/ptodata/1/pubnra/US10B_PUBCOMB.seq/*
 5: /cgn2_6/ptodata/1/pubnra/US10A_PUBCOMB.seq/*
 6: /cgn2_6/ptodata/1/pubnra/US10B_PUBCOMB.seq/*
 7: /cgn2_6/ptodata/1/pubnra/US10C_PUBCOMB.seq/*
 8: /cgn2_6/ptodata/1/pubnra/US10D_PUBCOMB.seq/*
 9: /cgn2_6/ptodata/1/pubnra/US10E_PUBCOMB.seq/*
 10: /cgn2_6/ptodata/1/pubnra/US11_FUBCOMB.seq/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Description
		%	ID
1	20	100.0	Sequence 5, Appli
2	20	100.0	Sequence 5, Appli
3	18	90.0	Sequence 1273, Appli
4	18	90.0	Sequence 36, Appli
c	5	18	Sequence 182, Appli
6	16	80.0	Sequence 1275, Appli
7	16	80.0	Sequence 79, Appli
8	16	80.0	Sequence 1274, Appli
c	9	15.8	Sequence 1274, Appli
c	10	15.8	Sequence 862259, Appli
c	11	15.8	Sequence 873649, Appli
c	12	15.2	Sequence 940468, Appli
c	13	15	Sequence 259831, Appli
c	14	14.8	Sequence 1274, Appli
c	15	14.4	Sequence 974400, Appli
c	16	14.4	Sequence 147123, Appli
c	17	14.4	Sequence 915488, Appli
c	18	14.4	Sequence 986433, Appli
c	19	14.2	Sequence 60, Appli
c	20	14.2	Sequence 64719, Appli
c	22	14.2	Sequence 103539, Appli
c	23	14.2	Sequence 585916, Appli

RESULT 1
US-10-220-033-5
 ; Sequence 5, Application US/10220033
 ; PUBLICATION NO. US20030186906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlingensiepen, Karl-Hermann
 ; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene and a molecule binding to an expression product of that gene
 ; TITLE OF INVENTION: Gene
 ; FILE REFERENCE: P68110US0
 ; CURRENT APPLICATION NUMBER: US/10/220,033
 ; CURRENT FILING DATE: 2003-03-17
 ; PRIORITY APPLICATION NUMBER: PCT/EP01/02694
 ; PRIOR FILING DATE: 2001-03-10
 ; PRIORITY APPLICATION NUMBER: EP00105190.3
 ; PRIOR FILING DATE: 2000-03-11
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: antisense
 ; OTHER INFORMATION: oligonucleotide
 US-10-220-033-5
 Query Match Score 20; DB 6; Length 20;
 Best_Local_Similarity 100.0%; Pred. No. 3.8;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 2
US-10-94-919-532
 ; Sequence 532, Application US/10984919
 ; Publication No. US20050130927A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlingensiepen, Karl-Hermann
 ; APPLICANT: Breyisch, Wolfgang
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 ; FILE REFERENCE: 10496/P63763USO

ALIGNMENTS

CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIORITY NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 532
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense Oligonucleotide
US-10-984-919-532

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3,8; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3,8; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3,8; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-984-919-1273
; Sequence 1273, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10996/P63763JSO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIORITY NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; NUMBER OF SEQ ID NOS: 1764
; SEQ ID NO: 1273
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense Oligonucleotide
US-10-984-919-1273

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-984-919-267-36
; Sequence 36, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: Antisense Oligonucleotide
; FILE REFERENCE: PCT/EP98/00497
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 1998-01-30
; PRIORITY NUMBER: EP 97 101 531.8
; NUMBER OF SEQ ID NOS: 1764
; LENGTH: 16
; TYPE: DNA

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PCT/EP98/00497
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO: 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-984-919-267-36

Query Match 90.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-10-984-919-267-182/C
; Sequence 182, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PCT/EP98/00497
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO: 182
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-984-919-267-182

Query Match 90.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 1 GCTTTCACCAATTGGAA 18
Db 3 GCTTTCACCAATTGGAA 20

Query Match 90.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 1 GCTTTCACCAATTGGAA 18
Db 18 GCTTTCACCAATTGGAA 1

RESULT 6
US-10-984-919-1275
; Sequence 1275, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Briesch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763JSO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIORITY NUMBER: US/09/341,700
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; NUMBER OF SEQ ID NOS: 1764
; SEQ ID NO: 1275
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense Oligonucleotide
US-10-984-919-1275

ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence:
 OTHER INFORMATION: antisense oligonucleotide
 US-10-984-919-1275

Query Match Score 16; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 5 TCACCAAATTGGAAAGC 20
 Db 1 TCACCAAATTGGAAAGC 16

RESULT 7
 US-10-146-058-79
 / Sequence 79, Application US/10146058
 / Publication No. US2003004049A1
 / GENERAL INFORMATION:
 / APPLICANT: Schlingensiepen, Georg-Ferdinand
 / APPLICANT: Schlingensiepen, Karl-Hermann
 / APPLICANT: Brysch, Wolfgang
 / APPLICANT: Schlingensiepen, Reimar
 / APPLICANT: Bogdahn, Ulrich
 TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
 TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
 NUMBER OF SEQUENCES: 137
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Jacobson, Price, Holman & Stern
 STREET: 400 Seventh St. N.W.
 CITY: Washington D.C.
 COUNTRY: U.S.A.
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/146,058
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/535,249
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 93 107 089.0
 FILING DATE: 30-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 93 107 849.7
 FILING DATE: 13-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Player, William E.
 REGISTRATION NUMBER: 31,409
 REFERENCE/DOCKET NUMBER: 10577/P58418
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 338-6666
 TELEFAX: (202) 393-5350
 TELEX: RCA 248593 IDEA UR
 INFORMATION FOR SEQ ID NO: 79:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 ANTI-SENSE: YES

Query Match Score 16; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 80 0% ; Score 16; DB 10; Length 25;
 Db 1 TCACCAAATTGGAAAGC 20

RESULT 8
 US-10-984-919-1215
 / Sequence 1215, Application US/10984919
 / Publication No. US2005013027A1
 / GENERAL INFORMATION:
 / APPLICANT: Schlingensiepen, Karl-Hermann
 / APPLICANT: Brysch, Wolfgang
 / TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 / FILE REFERENCE: 10496/P63763USO
 / CURRENT APPLICATION NUMBER: US/10/984,919
 / CURRENT FILING DATE: 2004-11-10
 / PRIOR APPLICATION NUMBER: US/08/341,700
 / PRIOR FILING DATE: 1999-05-24
 / PRIOR APPLICATION NUMBER: PCT/EP98/00497
 / PRIOR FILING DATE: 1998-01-30
 / PRIOR APPLICATION NUMBER: EP 97 101 531.8
 / PRIOR FILING DATE: 1997-01-31
 / NUMBER OF SEQ ID NOS: 1764
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 1215
 / LENGTH: 18
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence:
 / OTHER INFORMATION: antisense Oligonucleotide
 US-10-984-919-1215

Query Match Score 16; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 5 TCACCAAATTGGAAAGC 20
 Db 1 TCACCAAATTGGAAAGC 16

RESULT 9
 US-11-036-317-862259/c
 / Sequence 862259, Application US/11033317
 / Publication No. US20050214923A1
 / GENERAL INFORMATION:
 / APPLICANT: Blume, John
 / TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 / FILE REFERENCE: 3654.1
 / CURRENT APPLICATION NUMBER: US/11/036,317
 / CURRENT FILING DATE: 2005-01-13
 / PRIOR APPLICATION NUMBER: US 60/536,639
 / PRIOR FILING DATE: 2004-01-13
 / NUMBER OF SEQ ID NOS: 99174
 / SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 / SEQ ID NO: 862259
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Mus musculus
 US-11-036-317-862259

Query Match Score 15.8; DB 10; Length 25;
 Best Local Similarity 89.5%; Pred. No. 5.7e-02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;

Qy 2 CTTCACCAAATTGGAAAGC 20
 Db 22 CTTCACCAAATTGGAAAGC 4

RESULT 10
 US-11-036-317-873649/c
 Sequence 973649, Application US/11036317
 Publication No. US20050214823A1
 GENERAL INFORMATION:
 APPLICANT: Blume, John
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 FILE REFERENCE: 3654.1
 CURRENT APPLICATION NUMBER: US/11/036,317
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: US/60/536,639
 PRIOR FILING DATE: 2004-01-13
 NUMBER OF SEQ ID NOS: 991174
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 873649
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-11-036-317-873649

Query Match 79.0%; Score 15.8; DB 10; Length 25;
 Best Local Similarity 89.5%; Pred. No. 5.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTTTCACCAATTGGAAAC 20
 Db 20 CTTCACCAAGTGGAGC 2

RESULT 11
 Sequence 940468, Application US/11036317
 Publication No. US20050214823A1
 GENERAL INFORMATION:
 APPLICANT: Williams, Alan
 APPLICANT: Blume, John
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 FILE REFERENCE: 3654.1
 CURRENT APPLICATION NUMBER: US/11/036,317
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: US/60/536,639
 PRIOR FILING DATE: 2004-01-13
 NUMBER OF SEQ ID NOS: 991174
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 940468
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-11-036-317-940468

Query Match 79.0%; Score 15.8; DB 10; Length 25;
 Best Local Similarity 89.5%; Pred. No. 5.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTTTCACCAATTGGAAAC 20
 Db 19 CTTCACCAAGTGGAGC 1

RESULT 12
 US-11-19-956-259831/c
 Sequence 259831, Application US/10719956
 Publication No. US20040146910A1
 GENERAL INFORMATION:
 APPLICANT: Xue Mei Zhou
 TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 FILE REFERENCE: 3527.1
 CURRENT APPLICATION NUMBER: US/10/719,956
 CURRENT FILING DATE: 2003-11-20
 PRIOR APPLICATION NUMBER: 60/427,836
 PRIOR FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 639466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 259831
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-10-719-956-259831

Query Match 76.0%; Score 15.2; DB 7; Length 25;
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTTCACCAATTGGAAAGC 20
 Db 23 GCTGTAGCAATTGAAAGC 4

RESULT 13
 US-10-984-919-1274
 ; Sequence 1274, Application US/10984919
 ; Publication No. US20050130927A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schillingensiepen, Karl-Hermann
 ; APPLICANT: Brysch, Wolfgang
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 ; FILE REFERENCE: 10496/P6233US0
 ; CURRENT FILING DATE: 2004-11-10
 ; PRIOR APPLICATION NUMBER: US/10/984,919
 ; PRIOR FILING DATE: 1999-09-24
 ; PRIOR APPLICATION NUMBER: PCT/EP98/00497
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: EP 97 101 531.8
 ; PRIOR FILING DATE: 1997-01-31
 ; NUMBER OF SEQ ID NOS: 1764
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1274
 ; LENGTH: 15
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: antisense oligonucleotide
 ; OTHER INFORMATION: antisense oligonucleotide
 ; US-10-984-919-1274

Query Match 75.0%; Score 15; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCAAATTGGAAAGC 20
 Db 1 CACCAAATTGGAAAGC 15

RESULT 14
 US-11-060-756-239401
 ; Sequence 239401, Application US/11060756
 ; Publication No. US2005021354A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 239401
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 ; US-11-060-756-239401

Query Match 74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CTTTCACAAATTGGAG 19
 ||||| ||||| |||||
Db 3 CTTTCACAAATTGGAG 20

RESULT 15
US-10-719-900-974400/C
Sequence 974400, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 974400
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-974400

Query Match 72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 TCACCAATGGAGC 20
 ||||| ||||| |||||
Db 19 TCACTAATGGAGC 4

Search completed: March 4, 2006, 07:04:14
Job time : 419.368 secs

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:42:16 ; Search time 861.632 Seconds
(without alignments)

Title: US-09-701-583A-9

Perfect score: 18 -

Sequence: 1 cggatgtctattttgtta 18

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1934910

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : GenEmbl:
1: gb ba:
2: gb_in:
3: gb_env:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pr:
9: gb_ro:
10: gb_sb:
11: gb_sy:
12: gb_un:
13: gb_vl:
14: gb_hrg:
15: gb_pl:
16: gb_sg:
17: gb_st:
18: gb_tv:
19: gb_xref:
20: gb_xref2:
21: gb_xref3:
22: gb_xref4:
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unclassified sequences.

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 AUTHORS Brysch, W.
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 JOURNAL Patent: WO 9833904-A 1209 06-AUG-1998;
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 Reference 1 (bases 1 to 18)
 Authors Schlingensiepen, K.H. and Brysch, W.
 Title An antisense oligonucleotide preparation method
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 BIODIAGNOSTIK GESSELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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 Authors Schlingensiepen, K.H. and Brysch, W.
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REFERENCE BD234905
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 Title A method for stimulating the immune system
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 BIODIAGNOSTIK GESSELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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 PI KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG BRYSCHE
 PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/00, A61P35/00, A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00
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 FT /organism="Homo sapiens (human)".
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"

ORIGIN Query Match Similarity 100.0%; Score 18; DB 6; Length 18;
 Best Local Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Version BD234905
 Definition Sequence 30 from Patent WO2005059133.
 Accession CS123679
 Key GI:70912172
 Keywords synthetic construct
 Source synthetic construct
 Organism synthetic construct
 Other Sequences: artificial sequences
 Reference 1
 Authors Schlingensiepen, K.H.
 Title Combination therapy associating a tgf-beta antagonist with a chemotherapeutic agent
 Journal Patent: WO 2005059133-A 30-JUN-2005;
 Antisense Pharma GmbH (DE)
 Features Source
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence: human TGF-beta antisense oligonucleotide"

RESULT 5
 CS123679
 Locus CS123679
 Definition Sequence 30 from Patent WO2005059133.
 Accession CS123679
 Key CS123679.1
 GI:70912172
 Keywords synthetic construct
 Source synthetic construct
 Organism synthetic construct
 Other Sequences: artificial sequences
 Reference 1
 Authors Schlingensiepen, K.H.
 Title Combination therapy associating a tgf-beta antagonist with a chemotherapeutic agent
 Journal Patent: WO 2005059133-A 30-JUN-2005;
 Antisense Pharma GmbH (DE)
 Features Source
 1..18
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Query Match Similarity 100.0%; Score 18; DB 6; Length 18;
 Best Local Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Version BD234905
 Definition A method for stimulating the immune system.
 Accession BD234905
 Keyword Homo sapiens (human)
 Source Homo sapiens
 Organism Homo sapiens

RESULT 4
 BD234905
 Locus BD234905
 Definition A method for stimulating the immune system.
 Accession BD234905
 Version JP 2002517434-A/9
 Keyword Homo sapiens (human)

RESULT 6

AR222815	AR232815	Sequence 72 from patent US 6455689.	18 bp	DNA	linear	PAT 20-DEC-2002		Homo sapiens (human)
LOCUS	DEFINITION	Sequence 72 from patent US 6455689.					SOURCE	Homo sapiens
ACCESSION	AR232815						ORGANISM	Homo sapiens
VERSION	AR232815.1	GI:27275153						Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 18)						REFERENCE	Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H. and Schlingensiepen,R.
AUTHORS	Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H., Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2 (tgf-b2)						AUTHORS	Bogdahn,U., Brysch,W., Schlingensiepen,R.
TITLE	Schlingensiepen,R. and Bogdahn,U						TITLE	Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2 (tgf-b2)
JOURNAL	Antisense-oligonucleotides for transforming growth factor -beta.						JOURNAL	Patent: EP 1008649-A 72 14-JUN-2000; BIOGNOSTIK GES (DB)
FEATURES	Patent: US 6455689-A 72 24-SEP-2002;						FEATURES	Location/Qualifiers
source	Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH; Gottingen; EPX;						source	1..18 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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	/organism="unknown"							
	/mol_type="genomic DNA"							
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	Matches 18; Conservative 0; Mismatches 0;						Mismatches 0;	
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Db	1 CGGCATGTCATTTCATA 18							
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LOCUS	DEFINITION	Sequence 9 from Patent WO9963975.				DEFINITION	Sequence 4 from Patent WO0168146.	
ACCESSION	AX008976					ACCESSION	AX252494	
VERSION	AX008976.1	GI:9996350				VERSION	AX252494.1	GI:15985765
SOURCE	Homo sapiens (human)					SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens					ORGANISM	Homo sapiens	
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.					REFERENCE	Schlingensiepen,K.H. and Schlingensiepen,R.	
AUTHORS	A method for stimulating the immune system					AUTHORS	Mixture comprising an inhibitor or suppressor of a gene and a molecule binding to an expression product of that gene	
TITLE	Patent: WO 9963975-A 9 16-DEC-1999;					TITLE	Patent: WO 0168146-A 4 20-SEP-2001;	
JOURNAL	BIOGNOSTIK GBS (DE); BRYNSCH WOLFGANG (DE); HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)					JOURNAL	Biognostik Gesellschaft fuer biomelekulare Diagnostik mbH (DE)	
FEATURES	Location/Qualifiers					FEATURES	Location/Qualifiers	
source	1..18					source	1..18 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	
ORIGIN	Query Match	Score 18; DB 6; Length 18;				ORIGIN	Query Match	100.0%; Score 18; DB 6; Length 18;
	Best Local Similarity 100.0%; Pred. No. 2.7e+02;						Best Local Similarity 100.0%; Pred. No. 2.7e+02;	
	Matches 18; Conservative 0; Mismatches 0;						Mismatches 0;	
Qy	1 CGGCATGTCATTTCATA 18						Indels 0;	Gaps 0;
Db	1 CGGCATGTCATTTCATA 18							
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LOCUS	DEFINITION	Sequence 72 from Patent EP1008649.				DEFINITION	Sequence 72 from Patent EP1160319.	
ACCESSION						ACCESSION	AX316431	
VERSION						VERSION	AX316431.1	GI:17899604
SOURCE	unidentified sequences					SOURCE	unidentified sequences	
ORGANISM	unclassified					ORGANISM	unclassified	

ORGANISM unidentified unclassified sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch, W. and Schlingensiepen, K.
JOURNAL AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 Patent: WO 9833904 -A 1277 06 -AUG-1998;
FEATURES BIONOSTIK GES (DE); BRYSCHE WOLFGANG (DE)
source Location/Qualifiers
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/organism='unidentified'
/mol type='unassigned DNA'
/db_xref="taxon:32644"

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Query Match 88.9%; Score 16; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3..1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTATTGG 16
Db 1 CGGCATGCTATTGG 16

RESULT 15
BD066642 BD066642 16 bp DNA linear PAT 27-AUG-2002
LC/CUS An antisense oligonucleotide Preparation method.
DEFINITION An antisense oligonucleotide Preparation method.
ACCESSION BD066642
VERSION BD066642.1 GI:22612245
KEYWORDS JP 2001511000-A/1277.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen, K. H. and Brysch, W.
TITLE An antisense oligonucleotide Preparation method
JOURNAL Patent: JP 2001511000-A 1277 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-P/1277
PD 07-AUG-2001
PP 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531..8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCHE
PC C12N15/11, C07H11/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..16
/organism='Unknown'.
FEATURES Location/Qualifiers
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/organism='unidentified'
/mol type='genomic DNA'
/db_xref="taxon:32644"

ORIGIN

Query Match 88.9%; Score 16; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3..1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTATTGG 16
Db 1 CGGCATGCTATTGG 16

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:32 ; Search time 69.1579 Seconds
 (without alignments)
 462.653 Million cell updates/sec

Title: US-09-701-583a-9
 Perfect score: 18
 Sequence: 1 cggcatgtctatttgtta 18

Scoring table: IDENTITY_NUC
 Gapext 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1198766

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA,*

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 3: /cggn2_6/pctodata/1/ina/6-B-COMB.seq: *
 4: /cggn2_6/pctodata/1/ina/6B-COMB.seq: *
 5: /cggn2_6/pctodata/1/ina/H-COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	18	100.0	18	US-09-535-249-72
2	13.8	76.7	20	Sequence 72, Appl
3	13.4	74.4	20	Sequence 29, Appl
4	13.2	73.3	25	Sequence 7, Appl
5	13.2	73.3	25	Sequence 19083, A
6	12.8	71.1	22	Sequence 72258, A
7	12.4	68.9	20	Sequence 254, App
8	12.4	68.9	20	Sequence 35, Appl
9	12.4	68.9	24	Sequence 21, Appl
10	12.2	67.8	18	Sequence 3, Appl
11	12.2	67.8	24	Sequence 1132, A
12	12.2	67.8	25	Sequence 9, Appl
13	12.2	67.8	31	Sequence 11, Appl
14	12.2	67.8	31	Sequence 113, App
15	12.2	67.8	31	Sequence 134, App
16	12.2	67.8	31	Sequence 134, App
17	12.2	67.8	31	Sequence 134, App
18	12.2	67.8	31	Sequence 113, App
19	12.2	67.8	31	Sequence 113, App
20	12.2	67.8	31	Sequence 113, App
21	12	66.7	27	Sequence 3, Appl
22	12	66.7	30	Sequence 65, Appl
23	11.8	65.6	15	Sequence 105, Appl
24	11.8	65.6	15	Sequence 631, App

ALIGNMENTS

RESULT 1
 US-09-535-249-72
 ; Sequence 72, Application US/08535249
 ; Patent No. 6455689

GENERAL INFORMATION:
 APPLICANT: Schillingensiepen, Georg-Ferdinand
 APPLICANT: Brysch, Wolfgang
 APPLICANT: Schillingensiepen, Karl-Hermann
 APPLICANT: Schillingensiepen, Reimar
 APPLICANT: Bogdani, Ulrich
 TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of immuno-suppressive effect of transforming-growth-factor beta
 NUMBER OF INVENTION: 1
 NUMBER OF SEQUENCES: 137
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jacobson, Price, Holman & Stern
 STREET: 400 Seventh St. N.W.
 CITY: Washington D.C.
 COUNTRY: U.S.A.
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,249

FILING DATE:
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 93 107 089.0
 FILING DATE: 30-APR-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 93 107 849.7
 FILING DATE: 13-MAY-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Player, William E.
 NAME: Player, William E.
 REGISTRATION NUMBER: 31,409
 REFERENCE/DOCKET NUMBER: 10577/P58418
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-6666
 TELEFAX: (202) 393-5350
 TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown

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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-72

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Best Local Similarity 100.0%; Pred. No. 7.3; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-06-429-322-39
; Sequence 29, Application US/09429322A
; Patent No. 6190869
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN KINASE C-THETA
; FILE REFERENCE: RTS-0100
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 601100,678
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO: 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
US-09-429-322-29

Query Match      76.7%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.4%; Pred. No. 9.7e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GGCATGTCTATTGTA 18
Db      2  ||||| ||||| 18

RESULT 3
US-10-053-662A-7
; Sequence 7, Application US/10053662A
; Patent No. 6916618
; GENERAL INFORMATION:
; APPLICANT: Alexandra Charlesworth
; APPLICANT: Falvina Spirito
; APPLICANT: Guerrino Meneguzzi
; APPLICANT: John Baird
; APPLICANT: Keith Linder
; TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
; TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
; FILE REFERENCE: P84USA4
; CURRENT APPLICATION NUMBER: US/10/053,662A
; CURRENT FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO: 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: primer
US-10-053-662A-7

Query Match      74.4%; Score 13.4; DB 3; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.6e-03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
US-09-396-196G-19083
; Sequence 19083, Application US/09396196G
; Patent No. 682174
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 601100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 128806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 19083
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-19083

Query Match      73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CGGCATGTCTATTGTA 18
Db      1  ||||| ||||| 15

RESULT 5
US-09-396-196G-72258/C
; Sequence 72258, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 601100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 72258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-72258

Query Match      73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CGGCATGTCTATTGTA 18
Db      1  ||||| ||||| 15

RESULT 6
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; Sequence 254, Application US/09526193A
; Sequence 254, Application US/09526193A

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TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSER_020CPI

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US 09/298,850

EARLIER FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER FILING DATE: 1998-11-23

EARLIER APPLICATION NUMBER: US 60/082,614

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO: 11332

LENGTH: 18

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: primer_bind

LOCATION: 1..18

OTHER INFORMATION: downstream amplification primer 99-4284 for SEQ 3467, in compleme

US-09-422-978-1132

RESULT 11

US-08-273-402B-9

Sequence 9, Application US/08273402B

Patent No. 558403

GENERAL INFORMATION:

APPLICANT: Strom, Terry

APPLICANT: Rubin-Kesly, Vicki E.

APPLICANT: Libermann, Towia

TITLE OF INVENTION: METHODS AND COMPOUNDS FOR

TITLE OF SEQUENCE: PREVENTION OF GRAFT REJECTION

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/273,402B

FILING DATE: 11-JUL-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/024,569

FILING DATE: 01-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/843,731

FILING DATE: 28-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Paul T. Clark, Esq.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 03311/012001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

Query Match 67.8%; Score 12.2; DB 3; Length 18;

Best Local Similarity 82.4%; Pred. No. 6.3e+03;

Matches 14; Conservative 0; Mismatches 3;

Indels 0; Gaps 0;

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Db 18 GGCACTACTTTGCA 2

RESULT 12

US-09-903-013-11

Sequence 11, Application US/09030313

Patent No. 6685950

GENERAL INFORMATION:

APPLICANT: Weber, Olaf

APPLICANT: Schlap, Tobias

APPLICANT: Sigling, Angela

APPLICANT: Knorr, Andreas

APPLICANT: Hirth-Biebrich, Claudia

APPLICANT: Theiss, Gudrun

TITLE OF INVENTION: Use of Scatins of Parapoxvirus Ovis for Producing Antiviral Medic

TITLE OF INVENTION: Use of Medicaments Against Cancer

FILE REFERENCE: LeA 34 376

CURRENT APPLICATION NUMBER: US/09/903,013

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: DE10033582.9

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: DE0122451.6

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 11

LENGTH: 25

TYPE: DNA

ORGANISM: Mus sp.

US-09-903-013-11

RESULT 13

US-08-823-516-113/C

Sequence 113, Application US/08823516

Patent No. 5994059

GENERAL INFORMATION:

APPLICANT: Hall, Jeff G.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Mast, Andrea L.

APPLICANT: Brow, Mary Ann D.

TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple

TITLE OF INVENTION: Sequential Invasive Cleavages

NUMBER OF SEQUENCES: 163

CORRESPONDENCE ADDRESS:

ADDRESSE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/823,516
 FILING DATE: 24-MAR-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/01072
 FILING DATE: 21-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/759,038
 FILING DATE: 02-DEC-1996
 APPLICATION NUMBER: US 08/758,314
 FILING DATE: 02-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/756,386
 FILING DATE: 29-NOV-1996
 APPLICATION NUMBER: US 08/682,853
 FILING DATE: 12-JUL-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/599,491
 FILING DATE: 24-JAN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: FORS-02736
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANGENESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 FEATURE:
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 LOCATION: replace(1..2, "")
 OTHER INFORMATION: /note= "The residues at these
 OTHER INFORMATION: positions are a 2'-deoxycytosine 5'-O-(1-Thiomonophosphate)."
 FEATURE:
 NAME/KEY: misc difference
 LOCATION: replace(3, "")
 OTHER INFORMATION: misc difference
 OTHER INFORMATION: position is a 2'-deoxythymidine 5'-O-(1-Thiomonophosphate)."
 FEATURE:
 NAME/KEY: misc difference
 LOCATION: replace(4..5, "")
 OTHER INFORMATION: /note= "The residues at these
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 LOCATION: replace(6..8, "")
 OTHER INFORMATION: /note= "The residues at these
 OTHER INFORMATION: positions are a 2'-deoxythymidine 5'-O-(1-Thiomonophosphate)."
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 LOCATION: replace(9, "")
 OTHER INFORMATION: /note= "The residue at this
 OTHER INFORMATION: position is a 2'-deoxyguanosine 5'-O-(1-Thiomonophosphate)."
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 NAME/KEY: misc difference
 LOCATION: replace(10, "")
 OTHER INFORMATION: /note= "The residue at this
 OTHER INFORMATION: position is a 2'-deoxythymidine 5'-O-(1-Thiomonophosphate)."
 US-08-823-516-113

Query Match 67.8%; Score 12.2; DB 2; Length 31;

OQ	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps	0;
Db	US-08-759-038-134/C	2	GGCATGTCATTGTA	18			
	; Sequence 134, Application US/08759038						
	; Patent No. 6090543						
	GENERAL INFORMATION:						
	APPLICANT: Prudent, James R.						
	ATTORNEY: Hall, Jeff G.						
	APPLICANT: Lyamichev, Victor I.						
	APPLICANT: Brow, Mary Ann D.						
	APPLICANT: Dahlberg, James E.						
	TITLE OF INVENTION: Cleavage of Nucleic Acids						
	NUMBER OF SEQUENCES: 134						
	CORRESPONDENCE ADDRESS:						
	ADDRESSEE: Medlen & Carroll, LLP						
	STREET: 220 Montgomery Street, Suite 2200						
	CITY: San Francisco						
	STATE: California						
	COUNTRY: United States of America						
	ZIP: 94104						
	COMPUTER READABLE FORM:						
	COMPUTER: IBM PC compatible						
	OPERATING SYSTEM: PC-DOS/MS-DOS						
	SOFTWARE: Patentin Release #1.0, Version #1.30						
	CURRENT APPLICATION DATA:						
	APPLICATION NUMBER: US/08/759,038						
	FILING DATE: 02-DEC-1996						
	CLASSIFICATION:						
	PRIOR APPLICATION DATA:						
	APPLICATION NUMBER: US 08/						
	FILING DATE: 22-NOV-1996						
	PRIOR APPLICATION DATA:						
	ATTORNEY/AGENT INFORMATION:						
	NAME: Ingolia, Diane E.						
	REGISTRATION NUMBER: 40,027						
	REFERENCE/DOCKET NUMBER: FORS-02574						
	TELECOMMUNICATION INFORMATION:						
	TELEPHONE: (415) 705-8410						
	TELEFAX: (415) 397-8338						
	INFORMATION FOR SEQ ID NO: 113:						
	SEQUENCE CHARACTERISTICS:						
	LENGTH: 31 base pairs						
	TYPE: nucleic acid						
	STRANGENESS: single						
	TOPOLOGY: linear						
	MOLECULE TYPE: other nucleic acid						
	DESCRIPTION: /desc = "DNA"						
	FEATURE:						
	NAME/KEY: misc difference						
	LOCATION: replace(1..2, "")						
	OTHER INFORMATION: /note= "The residues at these						
	OTHER INFORMATION: positions are a 2'-deoxycytosine 5'-O-(1-Thiomonophosphate)."						
	FEATURE:						
	NAME/KEY: misc difference						
	LOCATION: replace(3, "")						
	OTHER INFORMATION: /note= "The residue at this						
	OTHER INFORMATION: position is a 2'-deoxythymidine 5'-O-(1-Thiomonophosphate)."						
	FEATURE:						
	NAME/KEY: misc difference						
	LOCATION: replace(4..5, "")						
	OTHER INFORMATION: position is a 2'-deoxythymidine 5'-O-(1-Thiomonophosphate)."						

OTHER INFORMATION: /note= "The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)."

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(6..8,"")

OTHER INFORMATION: /note= "The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)."

OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(10, "")

OTHER INFORMATION: /note= "The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."

OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."

Query Match: 67.8%; Score 12.2; DB 3; Length 31;
 Best Local Similarity 82.4%; Pred. No. 6.4e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGCATGCTTATTGTA 18
 Db 31 GGGCTGTATTGTA 15

RESULT 15

Sequence 134, Application US/08758314

PATENT NO. 6690605

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyanichay, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Improved Cleavage Agents

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,314

FILING DATE: 02-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/

FILING DATE: 29-NOV-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,853

FILING DATE: 12-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/599,491

FILING DATE: 24-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FDRS-02575

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 134:

SEQUENCER CHARACTERISTICS:

LENGTH: 31 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(1..2, "")

OTHER INFORMATION: /note= "The residues at these positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(3, "")

OTHER INFORMATION: /note= "The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(4..5, "")

OTHER INFORMATION: /note= "The residues at these positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(6..8, "")

OTHER INFORMATION: /note= "The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)."

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(9, "")

OTHER INFORMATION: /note= "The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."

FEATURE: misc_difference

NAME/KEY: misc_difference

LOCATION: replace(10, "")

OTHER INFORMATION: /note= "The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."

OTHER INFORMATION: position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."

Query Match: 67.8%; Score 12.2; DB 3; Length 31;
 Best Local Similarity 82.4%; Pred. No. 6.4e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGCATGCTTATTGTA 18
 Db 31 GGGCTGTATTGTA 15

Search completed: March 4, 2006, 02:07:27
 Job time : 70.1579 secs